SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) NAME: Innogenetics sa.
 - (B) STREET: Industriepark Zwijnaarde 7, box 4
 - (C) CITY: Gheat
 - (E) COUNTRY: Belgium
 - (F) POSTAL CODE (ZIP): B-9052
 - (G) TELEPHONE: 00 32 9 241 07 11
 - (H) TELEFAX: 00 32 9 241 07 99
- (ii) TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy.
- (111) NUMBER OF SEQUENCES: 270
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (111) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: BR34-4-20
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..213
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
- CTC ACG GAA CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly

 1 5 10 15
- GCC CAG TGT GGT TAT CGC CGC TGC CGT GCC AGT GGA GTT CTG CCT ACC
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr

002180.E9380 PCT/EP94/01323

20

AGC TTC GGC AAC ACA ATC ACT TGC TAC ATC AAG GCC ACA GCG GCT GCA Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 144

30

40

AGG GCC GCA GGC CTC CGG AAC CCG GAC TIT CTT GTC TGC GGA GAT GAT 192 Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp

96

CTG GTC GTG GTG GCT GAG AGT Leu Val Val Val Ala Glu Ser

35

213

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPCLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Ash Ser Lys Gly 10

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 40

Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp

Leu Val Val Val Ala Glu Ser 63

- (2) INFORMATION FOR SEQ ID NO: 3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (Vii) IMMEDIATE SOURCE:
 - (B) CLONE: BR36-23-18
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..213

| (xi) | SEQUENCE | DESCRIPTION: | SEQ | ID | NO: | 3: | |
|------|----------|--------------|-----|----|-----|----|--|
|------|----------|--------------|-----|----|-----|----|--|

CTC ACG GAA CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG 48 Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly GCC CAG TGT GGT TAT CGC CGC TGC CGT GCC AGT GGA GTT CTG CCT ACC 96 Ala Gin Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr 25 AGO TTO GGO AAC ACA ATO ACT TGO TAC ATO AAG GOO ACA GOG GOT GOA 144 Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 40 AGG GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT 192 Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp 55 213 CTG GTC GTG GTG GCT GAG AGT Leu Val Val Val Ala Glu Ser

- (2) INFORMATION FOR SEQ ID NC: 4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
1 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 35 40 45

Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp 50 55 60

Leu Val Val Val Ala Glu Ser 65 70

- (2) INFORMATION FOR SEQ ID NO: 5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPCLOGY: linear

| 98 | |
|--|------|
| (ii) MOLECULE TYPE: CDNA | |
| (iii) HYPOTHETICAL: NO | |
| (iii) ANTI-SENSE: NO | |
| (Vii) IMMEDIATE SOURCE: (B) CLONE: BR36-23-18 | |
| (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1213 | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: | |
| CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTT AAC AGC AAG GGG Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly 1 5 10 15 | - 48 |
| GCC CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr 20 25 30 | . 96 |
| AGC TTC GGC AAC ACA ATC ACT TGT TAC ATC AAA GCC ACA GCG GCC GCA Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 35 40 45 | 14÷ |
| AAA GCC GCA GGC CTC CGG AGC CCG GAC TTT CTT GTC TGC GGA GAT GAT AYS Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp 50 55 60 TG GTC GTG GTG GCT GAG AGT | 192 |
| eu Val Val Ala Glu Ser 65 70 | 213 |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 71 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: protein | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6: | |

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly

1 5 10 15

Ala Glm Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr

Ser Phe Gly Asn Thr lie Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 35 40 45

PCT/EP94/01323

Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp 50 55 60.

Leu Val Val Val Ala Glu Ser 65 70

- (2) INFORMATION FOR SEQ ID NO: 7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: BR36-23-20
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LCCATION: 1..213
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTT AAC AGC AAA GGG
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
1 5 10 15

GCC CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
20 25 30

AGC TTC GGC AAC ACA ATC ACT TGT TAC ATC AAA GCC ACA GCG GCC GCA 144
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala
35 40 45

AAA GCC GCA GGC CTC CGG AGC CCG GAC TTT CTT GTC TGC GGA GAT GAT
Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp
50 55 60

CTG GTC GTG GCT GAG AGT
Leu Val Val Ala Glu Ser
65 70

- (2) INFORMATION FOR SEQ ID NO: 8:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asm Ser Lys Gly
1 5 10 15

Ala Gla Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr

Ser Phe Gly Asm Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 35

Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp 50 55 60

Leu Val Val Val Ala Glu Ser 65 70

- (2) INFORMATION FOR SEQ ID NC: 9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: .cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:
 - (3) CLONE: BR33-2-17
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..213
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly

1 5 10 15

GCC CAG TGT GGT TAT CGC CGT TGT CGT GCC AGT GGA GTT CTG CCT ACC
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr
20 25 30

AGT TTC GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA GCG GCT GCA

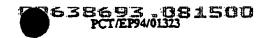
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala

35

40

45

AAA GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTT TGC GGA GAT GAT 193



Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp so 55 60

TTG GTC GTG GTG GCT GAG AGT Leu Val Val Val Ala Glu Ser 65 70 213

- (2) INFORMATION FOR SEQ ID NO: 10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTE: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
1 5 10 15

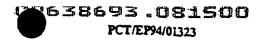
Ala Glm Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 35 40 45

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp 50 55 60

Leu Val Val Val Ala Glu Ser 65 70

- (2) INFORMATION FOR SEQ ID NO: 11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 213 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: BR33-2-21
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..213
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:



| CTC Leu 1 | ACG Thr | GAG Glu | CGG Arg | CTT Leu 5 | TAC | TGC Cys | GGG | GCC | Pro 10 | ATG Met | TIC | AAC Asti | AGC Ser | AAG Lys 15 | GGG Gly | 48 |
|-----------------|------------|------------|--------------------------------|-----------------|-----------|------------|------------|------------|------------|------------|------------------|-------------|------------|------------------|------------|-----|
| AGT | TTC | GGC | GGT Gly 20 AAC Asn | ACA | ATC | ACT | Cys | 25 TAC | Aža | Ser | Gly | Val | Leu 30 | Pro | Thr | 96 |
| 2,3 | 50 | ALA. | GGC Gly GTG | reu | Arg | AS:1 | Pro Pro | Asp | TTT Phe | CTT Leu | GTT Val 60 | TGC Cys | GGA Gly | gat Asp | GAT Asp | 192 |
| Leu 63 | Val | Val | Val | Ala | Glu 70 | Ser | | | | | | | | | | 213 |

- (2) INFORMATION FOR SEQ ID NO: 12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amine acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly
1 5 10

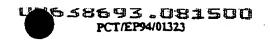
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala 35 40 45

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp 50 55 60

Leu Val Val Val Ala Glu Ser

- (2) INFORMATION FOR SEQ ID NO: 13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO



(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-5

(ix) FEATURE:

(A) NAME/KEY: CDS (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

| (XI) SEQUENCE DESCRIPTION. DBQ IS NO. IS. | |
|---|------|
| C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly 1 5 10 15 | 46 |
| GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC Val Arg Ala Leu Glu Asp Gly Ile Asm Phe Ala Thr Gly Asm Leu Pro 20 25 30 | - 94 |
| GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile 40 45 | 142 |
| CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAT GTC His Pro Ala Ala Ser Leu Glu Trp Arg Ash Thr Ser Gly Leu Tyr Val 50 55 60 | 190 |
| CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp 65 70 75 | 238 |
| GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Glm Asp Gly Asm 80 85 90 95 | 296 |
| ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr 100 105 110 | 334 |
| GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATG TTG GTG Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Met Leu Val 115 120 125 | 382 |
| GGC GCG GCC ACG ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly 130 135 140 | 430 |
| GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His 145 | 478 |
| CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly Ris Leu Ser 160 165 170 175 | 526 |

GGA CAC CGA ATG GCT Gly His Arg Met Ala 180

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- (2) INFORMATION FOR SEQ ID NO: 14:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MCLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
- Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
- Arg Ala Leu Glu Asp Gly Ile Asm Phe Ala Thr Gly Asm Leu Pro Gly 20 25 30
- Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His
- Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60
- Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80

 Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr 85 90
- Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
- Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Met Leu Val Gly
- Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 135 140
- Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln 155 150 155 160
- Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly 165 170 175

His Arg Met Ala

- (2) INFORMATION FOR SEQ ID NO: 15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

| (| ii) | MOLE | CULE | TYP | PE: 0 | ena | | | | | | | | | | | |
|------------|------------------|-------------------|---------------------|-------------------|---------------------------------|-------------------|----------------------|-------------------|------------------|------------|------------------|-------------------|-------------------|---------------------|------------|------|-----|
| (i | .ii) | HYPC | THE | ICAL | .: NC | • | | | | | | | | | | | |
| (1 | .ii) | ANT | -SEN | ISE : | NO | | | | | | | | | | | | |
| (v | rii) | | DIAT CLC | | | | .4 | | | | | | | | | | |
| (| (1x) | (A) | TURE: NAM LOC | Œ/K | | | 12 | | | | | | | | | | |
| 1 | (xi) | SEQ | UENC: | E DE | SCRI | PTION | 1: S | eg II | D NO | : 15 | : | | | | | | |
| | GG L G1 | y al | r cc: a Pr: | o Va | A GG: 1 Gl [.] 5 | A GGG y Gl; | GT: Y Va | C GC. | a Ar | g li | S CT a Le | GCC u Ala | G CA | r GG: s Gl: 1 | Y | - 46 | |
| GTG / | agg Azg | GCC Ala | CTT (Leu (| GAA Glu 20 | GAC (| GGG : Gly : | ATA Ile | AAT Asn | TTC Phe 25 | GCA Ala | ACA Thr | GGG A | AAT Asn | TTG Leu 30 | Pro CCC | 94 | |
| GGT Gly | TGC Cys | TCC Ser | TTT Phe | TCT Ser | ATC Ile | TTC : Phe | C Leu | CCT Pro 40 | GCT Ala | CTG Leu | TTC Phe | TCT Ser | TGC Cys 45 | TTA Leu | ATC Ile | 142 | |
| CAT His | CCA Pro | GCA Ala 50 | GCT Ala | AGT Ser | CTA Leu | GAG Glu | TGG T=TP 55 | CGG Arg | AAC Asn | ACG Thr | TCT Ser | GGC Gly 60 | CTC | TAT Tyt | GTC Val | 190 | } |
| CTT Leu | ACC Thr 65 | AAC Asn | GAC Asp | TGT Cys | TCC Ser | አአፒ አร። 70 | AGC Ser | AGT Ser | ATT Ile | GTG Val | TAT Tyr 75 | GAG Glu | GCC Ala | GAT ÇEK | GAC Asp | 239 | 3 |
| Val | Ile | Leu | CAC His | Thr | Pro 85 | Gly | Cys | Val | Pro | Cys | Va. | Gln | Asp | Gly | Asn 95 | 28 | 6 |
| ACA | TCT Ser | GCG Ala | TGC Cys | 100 Lab Leg | ACC | CCA Pro | GTG Val | ACA Thr | Pro 105 | Thr | GTG Val | GCA Ala | GTC Val | AGG Arg 110 | IÀI | 33 | ÷ |
| GTC Val | GGA Gly | GCA Ala | ACC Thr 115 | ACC Thr | GCT Ala | TCG Ser | ATA Ile | CGC Arg 120 | Arg | CAT His | GTA Val | GAC Asp | ATA Ile 125 | Leu | GTG Val | 38 | 2 |
| GGC Gly | GCG Ala | GCC Ala 130 | Thr | ATG Met | TGC Cys | TCT Ser | GCT Ala 135 | Leu | TAC | GTG Val | GGT Gly | GAT Asp 140 | Met | TGI Cys | Gly | 43 | 0 |
| GCC Ala | GTC Val | Phe | CTC Leu | GTG Val | GGA Gly | CAA Gln 150 | Ala | TTC Phe | ACG The | TTC Phe | 155 | Pro | CG? | CGC | CAT His | 4 | 7 9 |

SUBSTITUTE SHEET (RULE 26)

CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA

Gla Thr Val Gla Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser 160 170 170

GGA CAC CGA ATG GCT Gly His Arg Mer Ala

541

- (2) INFORMATION FOR SEQ ID NO: 16:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 190 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
- Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val
- Arg Ala Leu Glu Asp Gly Ile Asm Phe Ala Thr Gly Asm Leu Pro Gly
- Cys Ser Phe Ser Ile Phe Leu Pro Ala Leu Phe Ser Cys Leu Ile His
- Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60
- Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80
- Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asm Thr
- Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
- Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val Gly
 115 120 125
- Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 130 135 140
- Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln 145 150 155 160
- Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
 165 170 175

His Arg Met Ala 190

- (2) INFORMATION FOR SEQ ID NO: 17:
 - (i) SEQUENCE CHARACTERISTICS:

| (A) | LENGTH: 541 base pairs |
|-----|------------------------|
| (3) | TYPE: nucleic acid |
| (C) | STRANDEDNESS: single |
| (D) | TOPOLOGY: linear |

(ii) MOLECULE TYPE: CDNA

(iii) HYPCTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE: (B) CLONE: HD10-2-21

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

| • | | - | | |
|---|-----------------|---|---|----|
| | | | cc crr GCS CAT GGC la Leu Ala His Gly 15 | 46 |
| | | | ACA GGG AAT TTG CC Thr Gly Asn Leu Pr 30 | |
| | e Ser Ile Phe I | | TTC TCT TGC TTA AT Phe Ser Cys Leu Il 45 | |
| | | | TOT GGC OTO TAC GT Ser Gly Leu Tyr Va 60 | |
| | | | TAT GAG GCC GAT GA Tyr Glu Ala Asp As 75 | |
| | | | GTT CAG GAC GGT AR Val Glm Asp Gly As | |
| | | | GTS GCA GTC AGG TA Val Ala Val Arg Ty 110 | |
| | r Thr Ala Ser | | GTA GAC ATA TIG GT Val Asp Ile Leu Vo 125 | |
| | r Met Cys Ser | | GGT GAT ATG TGT GG Gly Asp Met Cys G 140 | |

| GCC Ala | GTC Val 145 | TTC Phe | CTC Leu | GTG Val | GGA Gly | CAA Gln 150 | GCC | TTC Phe | ACG Thr | TTC Phe | AGA Arg 155 | SE CCI | Arg | CGC | CAT His | 478 |
|-------------------|-------------------|------------|------------|------------|-------------------|-------------------|------------|------------|------------|-------------------|---|------------|------------|------------|-------------------|-----|
| CAA Gln 160 | ACG Thr | GTC Val | CAG Gln | ACC Thr | TGT Cys 165 | AAC Asn | TGC Cys | TCA Ser | CTG Leu | TAC Tyr 170 | S S S S S S S S S S S S S S S S S S S | GGC Gly | CAT His | CTT Leu | TCA Ser 175 | 526 |
| GGA Gly | | | ATG Met | | | | | | | | | | | | | 541 |

(2) INFORMATION FOR SEQ ID NO: 18:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: procein
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val

Arg Ala Leu Glu Asp Gly Ile Asm Phe Ala Thr Gly Asm Leu Pro Gly 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80

Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr

Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val

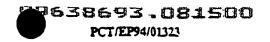
Gly Ala Thr Thr Ala Ser Ile Arg Arg Eis Val Asp Ile Leu Val Gly
115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 130 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly
165 170 175

His Arg Met Ala

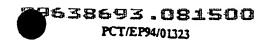


| (2) | INFO | RMAT | CION | FOR | SZQ | ID N | 0: 1 | 9 : | | | | | | | | |
|-----------|-------|-------------------|-------------------------|-------------|--------------|--------------------------------------|----------------------|----------|------------|-----------|------|------|------|-------------|-----------------|-----|
| | (i) | (A) (B) (C) | () LE () TY () ST | NGTH PE: | : 54 nucl | TERI 1 ba .eic .SS: 1ine | se p acid sing | airs | ŧ | | | | | | | |
| | (ii) | MOL | ECUL | e Ti | PE: | CONA | • | , | | | | | | | | |
| | (111) | HYP | OTHE | TICA | I: N | rc o | | | | | | | • | | | |
| | (111) | ANT | :I-SZ | : Eek | NO | | | | | | | | | | | |
| | (vii) | | | | | Ξ: 16-9- | 13 | | | | | | | | | |
| | (ix) | | TURE | | ·=v. | CDS | | | | | | | | | | |
| | | | | | | 25 | 41 | | | | | | | | | |
| | (yi) | 570 | אנ וביצור | יה חי | י ברוף | PTIC | ·X | FO T | סגי הי | . 10 | ١. | | | | | |
| c g | | | - | | | ià Go | | | | | | T GO | e ca | er Ge | ic | 45 |
| | | | | | | y Gi | | | la Az | | | | | .s G1 | | |
| | | | | | | GGG Gly | | | | | | | | | CCC | 94 |
| | 3 | | | 20 | , | | | | 25 | | •••• | , | | 30 | | |
| | | | | | | TTC Phe | | | | | | | | | ATT Ile | 142 |
| ••• | -, - | | 35 | | | | | 40 | | | | | 45 | | | |
| | | | | | | GAG Glu | | | | | | | | | GTC Val | 190 |
| 0 | | 50 | | ••• | | • | 55 | | | | | 60 | | -,- | | |
| | | | | | | AAT Asn | | | | | | | | | | 238 |
| Leu | 65 | ASI | ASP | Cys | ser | 70 | 361 | Ser | 114 | vai | 75 | GIU | ALA | ASP | AS ₂ | |
| | | | | | | | | | | | | | | | AAT | 285 |
| Val 80 | Ile | Leu | His | Thr | Pro 85 | Gly | Cys | ITE | PIO | Cys 90 | val | Gin | Asp | GTÅ | Asn 95 | • |
| | | | | | | | | | | | | | | | TAC | 334 |
| Thr | Ser | Thr | Cys | 100 | Thr | Pro | Val | Thr | Pro 105 | Thr | Val | Ala | Val | Lys 110 | īyr | |
| GTO | GGS | CCD | ».cc | 200 | CCT | TCG | 3773 | - CGC | AGT | CET | GTG | G)C | СТА | 7 73 | GTG | 382 |

SUBSTITUTE SHEET (RULE 26)

Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val 120

115



| GGC | GCG Ala | GCC Ala 130 | 4 +++ | ATG Met | TGC | TCA Ser | GCG Ala 135 | CTC | TAC | GTG Val | GGT Gly | GAT Asp 140 | ATG Mec | TGT Cys | GGG Gly | | 430 |
|-------------------|-------------------|-------------------|------------|------------|-------------------|-------------------|-------------------|------------|------------|-------------------|-------------------|-------------------|------------|------------|-------------------|---|-----|
| GCC Ala | GTC Val 145 | TTC Phe | CTT | GTG Val | GGA Gly | CAA Gln 150 | GCC Ala | TTC Phe | ACG Thr | TTC Phe | AGA Arg 155 | CCT Pro | CGT Arg | CGC Arg | CAT His | | 478 |
| CAA Gin 160 | ACG Thr | GTC Val | CAG Gla | ACC Thr | TGT Cys 163 | AAC Asn | TGC Cys | TCG Ser | CTG Leu | TAC Tyr 170 | CCA Pro | GGC Gly | CAT His | CTT Leu | TCA Ser 175 | | 525 |
| GGA Gly | | | | | | | | | | | | | | | | ; | 541 |

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amine acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20: Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His 35 40 45

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80

Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln 145 150 155 160

Thr Val Gln Thr Cys Asm Cys Ser Leu Tyr Pro Gly His Leu Ser Gly

PCT/EP94/01323

165 170 175

| His | Arg | Mec | Ala |
|-----|-----|-----|-----|
| | | | 120 |

| (2) | INFORMATION | FOR | SEO | ID | NO: | 21. |
|-----|-------------|-----|-----|----|-----|-----|

(i) SEQUENCE CHAPACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-9-20

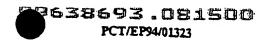
(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC

| Val Gly A | la Pro Val Gly G | ly Val Ala Arg A | la Leu Ala His Gly | |
|--------------|------------------|------------------|---------------------|--------|
| 1 | 5 | 10 | 15 | |
| | | | 101 000 117 000 000 | 94 |
| | | | ACA GGG AAT TTG CC | - |
| va: Arg Ala | | | Thr Gly Asn Leu Pro | • |
| | 20 | 25 | 30 | |
| GGT TGC TCC | TTT TCT ATT TTC | CIT CIT GCT CTG | TTC TCT TGC TTA AT | 142 |
| Gly Cys Ser | Phe Ser Ile Phe | Leu Leu Ala Leu | Phe Ser Cys Leu Il | e |
| | 35 | 40 | 45 | |
| | | | | |
| CAT CCA GCA | GCT AGT CTA GAG | TGG CGG AAT ACG | TCT GGC CTC TAT GT | C 190 |
| His Pro Ala | Ala Ser Leu Glu | Tro Arg Asa Thr | Ser Gly Leu Tyr Va | 1 |
| 50 | | 55 | 60 | |
| | | | | |
| | | | TAC GAG GCC GAT GA | |
| | | | Tyr Glu Ala Asp As | 3 |
| 65 | 70 | • | 75 | |
| GTT ATT CTG | CAC ACA CCC GGC | TGC ATA CCT TGT | GTC CAG GAC GGC AA | T 286 |
| Val Ile Leu | His Thr Pro Gly | Cys Ile Pro Cys | Val Gin Asp Gly As | a . |
| 80 | 85 | 90 | 9 | 5 |
| | | - | | |
| ACA TCC ACG | TGC TGG ACC CCA | GTG ACA CCT ACA | GTG GCA GTC AAG TA | .C 334 |
| Thr. Ser Thr | Cys Trp Thr Pro | Val Thr Pro Th | Val Ala Val Lys Ty | T |
| | 100 | 105 | 110 | |



| Val | GGA Gly | Ala | ACC Thr 115 | ACC | GCT Ala | TC3 Ser | ATA Ile | CGC Arg 120 | Ser | CAT His | GTG Val | GAC Asp | CTA Leu 125 | TTA Leu | GTG Val | | 382 |
|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|---|-----|
| Gly | GCG Ala | GCC Ala 130 | * * * * | ATG Met | TGC Cys | TCT Ser | GCG Ala 135 | CTC | TAC | GTG Val | GGT Gly | GAC Asp 140 | ATG Met | TGT Cys | GGG Gly | | 430 |
| GCT Ala | GTC Val 145 | TTC Phe | CTC | GTG Val | GGA Gly | CAA Glm 150 | gcc Ala | TTC Phe | ACG Thr | TTC Phe | AGA Arg 155 | Pro CCI | CGT Arg | CGC Arg | CAT His | | 478 |
| CAA Gln 160 | ACG Thr | GTC Val | CAG Gln | ACC Thr | TGT Cys 165 | AAC Asn | TGC Cys | TCG Ser | CTG Leu | TAC Tyr 170 | CCA Pro | GGC GGC | CAT His | CTT Leu | TCA Ser 175 | | 526 |
| GGA Gly | | | | | | | | | - | | | | • | | | • | 541 |

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55 60

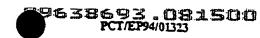
Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80

Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly
115 120 - 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 130 140



| | | | | | | | | • | •• | | | | | | | | |
|------------|-------|----------|---|------------------------|---------------|-----------------------|--------------|------------|------------|---------------|-----|-----|-----|------------|------------|----|-----|
| Val 145 | Phe | Leu | Val | Gly | Gla 150 | Ala | Phe | Thr | Phe | Arg 155 | Pro | Arg | Arg | His | Gla 160 | | |
| Thr | Val | Gln | Thr | Су з 165 | Asn | Cis | Ser | Leu | Tyr 170 | Pro | Gly | His | Leu | Ser 175 | Gly | | |
| His | Arg | Mec | Ala 190 | | | | | | | | | | | | | | |
| (2) | INFO | RMA: | KOIT | FCR | SEQ | ID % | IG: 2 | 23: | | | | | | | | | |
| | (\$) | (3 (5 | (UE)(() LE () T) () S1 () T(| ngt: (Pe : Trani | i: 54 nucl | il ba Leis ESS: | se g acid | pairs i | i . | | | | | | | | |
| , | (11) | MOI | LECII | E T | ?E: | CDNA | | | | | | | | | | • | |
| | (iii) | HYE | CTHE | TIC | د :ت | IC | | | | | | | • | | | | |
| | (iii) | ANT | FI-SE | NSE: | NC | | • | • | | | | | | | | | |
| | (vii) | | ŒDL; 3) CI | | | | -10 | | | | | | | | | *• | |
| | (ix) | () | ATURI A) NI B) LO | ME/I | | | 541 | | | | | | | | | | |
| | (xi) | SEC | 30231C | E Di | ESCR: | :77:0 | ON: S | SEQ I | D N |): 2 : | 3: | | | | | | |
| | | | CT CC | | | | | | la A | | | | | s G | | | 4€ |
| | | | CTT Leu | | | | | | | | | | | | | | 94 |
| | | | TTT Phe 35 | | | | | | | | | | | | | | 142 |
| | | | GCT Ala | | | | | Arg | | | | | | | GTC Val | | 190 |
| | | | GAC Asp | | | | | | | | | Glu | | | GAC Asp | | 238 |
| GTT | ATT | СТС | CAC | GCG | CCC | GGC | TGT | GTA | ССТ | TGT | GTC | CAG | GAC | GGC | : AAT | | 235 |

SUBSTITUTE SHEET (RULE 26)

90

Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn

85

9638693.081500 PCT/EP94/0123

| ACC The | Ser | Th: | TGC Cys | 100 Erp | ing | CCX erg | GTA Val | ACA Thr | Pro 105 | Thr | GTG Val | GCA Ala | GTC Val | AGG Arg 110 | TAC Tyr | 334 |
|--------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|---------------------|--------------|
| GTC Val | GGG | GCA Ala | ACC Thr 115 | Thr | GCT Ala | TCG Ser | ATA Ile | CGC Arg 120 | AGT Ser | CAT Kis | GTG Val | GAC Asp | CTG Leu 125 | TTA Leu | GTA Val | 382 |
| GCC | GCG Ala | GCC Ala 130 | ACG Thr | ATG Met | TGC Cys | TCT Ser | GCG Xla 135 | CIT | TAC Tyr | GTG Vai | ejà eei | GAT Asp 140 | ATG Met | TGT Cys | GGG Gly | 430 |
| GCC Ala | GTC Val 145 | TTC Phe | CTC Leu | GTG Val | GGA Gly | CAA Gla 150 | GCC Ala | TTC Phe | ACG Thr | TTC Phe | AGA Arg 155 | ccc Pro | CGC Arg | CGC Arg | CAT His | 478 |
| CAA Gl:: 160 | ACG Thr | GTC Val | CAG Glm | ACC Thr | TGT Cys 163 | AAC Asa | TGC Cys | TCG Ser | CTG Leu | TAC Tyt 170 | CCA Pro | GGC Gly | CAT His | Leu | TCA Ser . 175 | \$ 26 |
| | | | ATG Me: | | | | | | | | | | | | | 541 |

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His 35 40 45

Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80

Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly

uy6346830081500

115 120

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala 135

115

Val Ph Leu Val Gly Glm Ala Phe Thr Phe Arg Pro Arg Arg His Glm 155

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly 170

His Arg Met Ala

180

- (2) INFORMATION FOR SEQ ID NO: 25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 541 base pairs
 - (3) TYPE: nucleic acid-
 - (C) STRANDEDNESS: single
 - (D) TOPCLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:

(B) CLONE: BR33-1-19

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..541
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:
- C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
- GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC 94 Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro 20
- GGT TGC TCT TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC 142 Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile 40
- CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC 190 His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val 53
- CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp 70 65 75



| GTT Val 80 | ile | ren CIG | CAC His | Ala | Pro 85 | GJ À GGC | TGT Cys | GTA Val | Pro | TGT Cys 90 | GTC Val | CAG Gln | A ⊅⊅ | GGC Gly | AAT Asn 95 | 286 |
|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| ACG Thr | TCT Ser | ACA Th: | TGC Cys | TGG Trp 100 | ACC Thr | CCY bi | GTA Val | ACA Thr | Pro 105 | ACA Thr | GTG Val | GCA Ala | GTC Val | AGG Arg 110 | TAC Tyr | 334 |
| GTC Val | GGG GLy | GCX Ala | ACC Thr 115 | ACC Thr | GCT ALa | TCG Ser | ATA Ile | CGC Arg 120 | AGT Ser | CAT Eis | GTG Val | GAC Asp | CTG Leu 125 | TTA Leu | GTA Val | 382 |
| G1y | GCG Ala | GCC Ala 130 | ACG Thr | ATG Mec | TGC Cys | TCT Ser | GCG Ala 135 | CTT Leu | TAC Ty= | GTG Val | GGT Gly | GAT Asp 140 | ATG Met | TGT Cys | GGG Gly | 430 |
| YTE | GTC Val 145 | TTC Phe | CTC Leu | GTG Val | GGA Gly | CAA Gla 150 | GCC Ala | TTC Phe | ACG Thr | TTC Phe | AGA Arg 155 | CCC Pro | CGC | CGC | CAT His | 478 |
| Gla 150 | ACG Thr | GTC Val | CAG Gln | ACC Thr | TGT Cys 165 | AAC Asn | TGC Cys | TCG Ser | Leu | TAC Tyr 170 | 510 510 | GGC Gly | CAT His | CIT | TCA Ser 175 | 525 |
| GGA (| | | | | | | | | | | | | | | | 541 |

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val 1 5 10 15

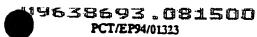
Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly
20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His 35 40 45 .

Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Giu Ala Asp Asp Val 65 70 75 80

The Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr 85 90 95



| | | | | | | | | 17 | | | | | | | |
|--------------------|--------------|---|----------------------|----------------------|----------------------|----------------------|----------------|----------------|------------|------------|------------|------------------|------------------|------------------|-----|
| Ser Th | r Cys | 100 | The | 320 | Val | Thr | Pro 105 | Thr | Val | Ala | Val | Arg 110 | - | · Val | |
| Gly Al | a Thr 115 | Thr | Ala | Ser | Ile | Arg 120 | Ser | His | Val | Asp | Leu 125 | | Val | Gly | • |
| Ala Ala 130 | a Thr | Mec | CYS | Ser | Ala 135 | Leu | Tyr | Val | Gly | Asp 140 | Mec | Суз | Gly | Ala | |
| Val Ph | e Leu | Vai | Gly | 51n 150 | λίa | ?he | Thr | Phe | Arg 155 | Pro | ۸zg | Arg | His | Gln 160 | |
| Thr Val | Gln | Thr | Cys 165 | Asn | Cys | Ser | Leu | Tyr 170 | Pro | Gly | His | Leu | Ser 175 | Gly | |
| His Arg | Met | Ala 180 | | | | | | | | | | | | | |
| (2) INE | ORMA: | PION | FOR | SEQ | ID N | rO: 2 | . 7 : | | | | | | | | - |
| (i | (C | QUENC A) LE B) TY C) ST C) TO | ngth Pe: Rand | : 54 nucl EDNE | l ba .eic :88: | se p acid sing | airs | • | | | | | | | |
| |) MCI | | | | | | | | | | | | | | |
| (iii |) HYE | OTHE | TICA | L: N | C | | | | | | | | | | |
| (iii |) ANI | :I-SE | NSE: | NC | | | | | • | | | | | | |
| (vii |) IMM | | | | | | | | | | | | | | |
| (ix | L) FEA |) CL TURE | | 33. | 3-1- | 20 | | | | | | | | | |
| | |) NA | | | | | | | | | | | | | |
| | (3 |) Lo | CATI | ON: | 25 | 41 | | | | | | | | | |
| (xi |) SEQ | UENC | E DES | SCRI | PTIO | N: 5 | EQ I | D %0 | : 27 | : | | | | | |
| C GTC G | SC GC | TCC | C GT | A GG. | A GG | C GT | د ود | a ag | A GC | c ct | T GC | G CA | T GO | ic . | 45 |
| Val G | ly Al | a Pro | | [G1; | y Gl | y Va. | 1 A1 | a کت 1 | | a Le | u Al | a Hi | | . y .5 | |
| GTG AGG Val Arg | GCC Ala | CTT (| GAG (Glu / 20 | asp (| GGG : | ATA : | AAC ' Asn ' | TTC (Phe : | GCA Ala | ACA (| GGG Gly | AAT Asn | TTG Leu 30 | CCC Pro | 94 |
| GGT TGC Gly Cys | TCT | TTT : Phe : | TCT A | ATC : | TTC (Phe 1 | CTT (Leu 1 | CTT (Leu : | GCT (Ala) | CTG Leu | TTC Phe | TCT Ser | TGC Cys 45 | TTA Leu | ATC Ile | 142 |

SUBSTITUTE SHEET (RULE 26)

60

CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC

His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val 55



| Leu | ACC Thr 65 | Asn | GAC A sp | TGT Cys | TCC Ser | AAT ASD 70 | AGT Ser | AGT Ser | ATT Ile | GTG Val | TAT Ty= 75 | GAG Glu | GCC Ala | GAT Asp | GAC Asp | 238 |
|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| GTT Val 80 | ATT Ile | CTG Leu | CAC Ris | GCS Ala | CCC Pro 88 | GGC Gly | TGT Cys | GTA Val | Pro | TGT Cys 90 | GTC Val | CAG Gln | GAC Asp | GGC Gly | AAT Asn 95 | 286 |
| ACS Thr | TCT Ser | ACA Thr | TGC Cys | TGG Trp 100 | ACC Thr | CCA Pro | GTA Val | ACA Thr | CCT Pro 105 | ACA Thr | GTG Val | GCA Ala | GTC Val | AGG Arg 110 | TAC Tyt | 334 |
| GTC Val | GGG Gly | GCA Ala | ACC Thr 115 | ACC Thr | GCT Ala | TCG Ser | ATA Ile | CGC Arg 120 | AGT Ser | CAT His | GTG Val | GAC Asp | CTG Leu 125 | TTX Leu | GTA Val | 382 |
| GGC Gly | GĊG Ala | GCC Ala 130 | ACG Thr | ATG Mes | TGC Cys | TCT Ser | GCG Ala 135 | CTT Leu | TAC Tyr | GTG Val | GGT Gly | GAT Asp 140 | ATG Met | TGT Cys | GGG Gly | 430 |
| GCC Ala | GTC Val 145 | TTC Phe | CTC Leu | GTG Val | GGA Glγ | CAA Gl:: 153 | GCC Ala | TTC Phe | ACG Thr | TTC Phe | AGA Arg 155 | SL2 CCC | CGC Arg | CGC | CAT His | 479 |
| CAA Gln 160 | ACG Thr | GTC Val | CAG Gln | ACC Thr | TGT Cys 165 | AAC Asa | TGC Cys | TCG Ser | CTG Leu | TAC Tyr 170 | CCA Pro | GGC Gly | CAT His | CTT Leu | TCA Ser 175 | 526 |
| GGA Gly | | | | | | | | | | | | | | | | 541 |

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val 1 5 10 15

Arg Ala Leu Glu Asp Gly Ile Asm Phe Ala Thr Gly Asm Leu Pro Gly 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His 35 40 45

Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu 50 55

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val 65 70 75 80

| Ile | Leu | His | ALE | 85 88 | Gly | Cys | Val | Pro | Cys 90 | Val | Gla | Asp | Gly | Asn 95 | Thr | |
|------------|------------|--------------|-------------------------|---------------------|---------------------------------------|-----------------------|--------------|------------|------------------|--------------------|------------|------------|--------------|------------------|------------------|-----|
| Ser | Thr | Суя | 100 | Thr | Pro | Val | Thr | Pro 105 | Thr | Val | Ala | | Arg 110 | Tyr | Val | |
| Gly | Ala | Thr 115 | The | Ala | Ser | Ile | Arg 120 | Ser | Eis | Val | Ysb | Leu 125 | Leu | Val | GŢĀ | |
| Als | Ala 130 | | Met | Суз | Ser | 135 | Leu | :\: | Val | Gly | كچې 140 | Mes | Cys | Gly | Ala | |
| Val 145 | Phe | Leu | Val | Gly | Gln 150 | ۲۱a | Phe | Thr | Phe | Arg 155 | Pro | yzā | Arg | His | Gln 160 | |
| Thr | Val | Gln | Thr | Cys 163 | Asn | C'ns | Ser | Leu | Ty= 170 | Pro | Gly | Ris | Leu | Ser 175 | Gly | |
| His . | Arg | Met | Ala 180 | | | | | | | | | | | | | • |
| (2) | INFC | RMAT | TON | FOR | SEQ | 12 N | ro : 2 | 29: | | | | | | | | |
| | (i) | R) E) | () LE () TY () SI | ngti Pe: Rani | iarac i: 28 nucl Edne Gy: | 17 ba .eic :SS: | se p acid | airs L | , | | | | | | | · |
| | (ii) | MOL | .zcvi | E T | Æ: | CENA | | | | | | | | | | |
| t: | iii) | HYP | OTHE | TIC | L: N | ic | | | | | | | | | | |
| (: | iii) | ANI | T-SE | NSE : | NO | | | | | | | | | | | |
| • (• | rii) | | | | OURC HCC | | i | • | | | | | | | | |
| | (ix) | (A | | ME/8 | EY: On: | | 87 | | | | | | | | | |
| | (xi) | SEQ | UENC | E DE | SCRI | PTIC | N: 5 | EQ I | D NO |): 29 |) : | | | | | • |
| TA G | sp P | TT T he T | دئ وو و | AG A | GC G Ser V | TC I | TC A | CT C | GA (Sly I | TA A eu 1 10 | CT (| CAC A | TA (le) | AT (| SCC Lla 15 | 47 |
| CAC 1 | rrr ?he | CTG Leu | TCA Ser | CAG Gln 20 | ACT Thr | AAG Lys | CAG Gla | CAG Gln | GGA Gly 25 | CTC Leu | AAC Asn | TTC Phe | TCG Ser | TTC Phe 30 | CTG Leu | 95 |
| ACT (| GCC | TAC | CAA | GCC | ACT | GTG | TGC | GCT | CGC | GCG | CAG | GCT | сст | ccc | CCA | 143 |

SUBSTITUTE SHEET (RULE 26)

45

191

Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro 40

AGT TGG GAC GAG ATG TGG AAG TGT CTC GTA CGG CTT AAG CCA ACA CTA

| Ser Trp Asp Glu Met | Trp Lys Cys Leu V | al Arg Leu Lys Pro Thr Leu |
|---------------------|-------------------|----------------------------|
| 50 | 5 5 | 60 |

CAT GGA CCT ACG CCT CTT CTA TAT CGG TTG GGG CCT GTC CAA AAT GAA
His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu
65 70 75

ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG GCA TGC ATG TCA

Lie Cys Leu Thr His Pro lie Thr Lys Tyr lie Met Ala Cys Met Ser

80 90 95

- (2) INFORMATION FOR SEQ ID NO: 30:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 1 5 10 15

Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr 20 25 30

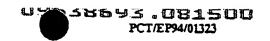
Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser 35 40 45

Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His 50 55

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Glm Asm Glu Ile 65 70 75 80

Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser 85 90 95

- (2) INFORMATION FOR SEQ ID NO: 31:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:
 (B) CLONE: HD10-1-25



| (ix) | FEATURE: |
|------|----------|
|------|----------|

(A) NAME/KEY: CDS
(B) LOCATION: 3..401

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

| | ,,,, | | | | | | | 354 | | · · | | | | | | | |
|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|-----|-----|
| TC | CAA Gla 1 | TAA Asa | gaa Glu | ATC Ile | TGC Cys 5 | TTG Leu | ACA Thr | CAC Eis | 310 CCC | GTC Val 10 | aca The | AAA Lys | TAC Tyr | ATT Ile | ATG Met 15 | | 47 |
| GCA Ala | TGC | ATG Met | TCA Ser | GC7 Als 20 | Asp | Leu | GAR Glu | GTA | ACC Thr 25 | The | AGC Se: | ACC Thr | TEP | GTG Val | TTG Leu | | 95 |
| CTT | GGA Gly | GGG Gly | GTC Val | Leu | GCG Ala | GCC Ala | CTA Leu | GCG Ala 40 | Ala | TAC | TGC Cys | : TTG : Leu | TCA Ser 45 | Val | GGC | - | L43 |
| TGC | GTT Val | GTA Val 50 | Ile | GTG Val | GGT Gly | CAT | Ile 55 | Glu | re | GGG G1y | GGC Gly | AAG Lys 60 | 510 | GCA Ala | CTC Leu | 2 | 191 |
| GTT Val | CCA Pro 65 | Asp | Lys | GAG Glu | GTG Val | TTG Leu 70 | Tyr | CAA Gln | CAG Gla | TAC | GAT Asp 75 | Glu | ATG Met | GAG Glu | GAG Glu | - 2 | 239 |
| TGC Cys 80 | TCG Ser | CAA Gln | GCC Ala | GCC Ala | CCA Pro 85 | TAC | ATC Ile | GAA Glu | CAA Gln | GCT Ala 90 | Gla | GTA Val | ATA | GCC Ala | CAC His 95 | 2 | 87 |
| CAG Glm | TTC Phe | AAG Lys | GAG Glu | AXA Lys 100 | Ile | CTT | GGA Gly | CTG Leu | CTG Leu 105 | CAG Gln | CGA | GCC Ala | ACC | CAA Glm 110 | CAA Gln | 2 | 335 |
| CAA Gla | GCT Ala | GTC Val | ATT Ile 115 | Glu | CCC Pro | GTA Val | ATA | GCT Ala 120 | TCC Ser | AAC Asn | TGG Try | CAA Gln | AAG Lys 125 | CTT | GAA Glu | 3 | 183 |
| | | | | | CAT His | | | | | | | | | | | 4 | 101 |

(2) INFORMATION FOR SEQ ID NO: 32:

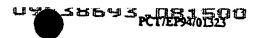
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met Ala 1 5 10 15



| Cys | Mec | Ser | Ala 20 | Asp | Leu | Glu | Val | Th= 25 | Thr | Ser | Thr | ırp | Val 30 | Leu | Leu | , |
|-------------|--------------------------------------|--|--|---|---|--|--------------|--------------------------|------------------|------------|------------|--------------|------------|------------------|-----------------|-----|
| Gly | Gly | Val 35 | Leu | Ala | Ala | Leu | Ala 40 | Ala | Tyr | Cys | Leu | Ser 45 | Val | Gly | Суз | |
| Val | Val 50 | Ile | Va: | Gly | His | Ile 55 | Glu | Leu | Gly | GĵÅ | Lys 60 | Pro | Ala | Leu | Val | |
| 9 <u>70</u> | Asp | Lys | Glu | Val | 70 | בורב | Gla | Gln | Tyr | ծsp 75 | Glu | Mec | Glu | Glu | Cys 80 | |
| Ser | Gln | Ala | Ala | Pro 85 | Tyr | Ile | Glu | Gln | Ala 90 | Gln | Val | Ile | Ala | His 95 | Gln | |
| Phe | Lys | Glu | Lys 100 | Ile | Leu | Gly | Leu | Leu 105 | Gla | Arg | λla | Thr | Gln 110 | Gla | Gln | |
| | | 115 | Glu Lys | | Val | Ile | Ala 120 | Ser | Asn | Įtp | Gla | Lys 125 | Leu | Glu | Thr | |
| | 130 | | ICN | | SEO | א כד | n. i | 13. | | | | | | | | |
| (| (ii) iii) iii) vii) (ix) | (A) (B) (C) (D) (D) (D) (D) (E) (E) (E) (E) (E) (E) (E) (E) (E) (E | PUENCE OF THE PU | NGTH PE: RAND POLO E TY TICA NSE: TE S ONE: ME/X CATI | E: 40 RUC1 PEDNE FGY: TE: N NO OURC HD1 EY: ON: | l ba eic SS: line CDNA CO | se pacid | airs : : : : | | . 33 | | | | | | |
| רכ כו | a a | AT G. | AA A' lu I | TC T | GC T | TG A | CA C | ac c | zo A CC C | TC A | .CAA | AA T Ys T | AC A | TT A | TG let 15 | 47 |
| CA (| IGC . | ATG ' | TCA (Ser) | GCT (Ala : 20 | GAT (Asp) | CTG : | GAA - Glu | GTA Val | ACC Thr 25 | ACC Thr | AGC Ser | ACC Thr | TEG | GTG Val 30 | TTG Leu | 95 |
| TT (| GGA (| GGG (| GTC (| CTC (| GCG (| GCC · | CTA | GCG | GCC | TAC | TGC | TTG | TCA | GTC | GGC | 143 |



| Leu | Gly | Gly | Val 35 | Leu | λia | Ala | Leu | Ala 40 | Ala | Tyr | Càs | Leu | Ser 45 | Val | Gly | |
|------------------|------------|------------------|-------------------|---------------------------------|------------------|------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|------------------------|------------------|-----|
| TGC Cys | GTT Val | GTA Val 50 | ATC Ile | GTG Val | GGT Gly | CAT His | ATC Ile 55 | GAG Glu | CTG Leu | GGG Gly | GGC Gly | AAG Lys 60 | 510 CC3 | GCA Ala | CTC Leu | 191 |
| GTT Val | Pro 65 | GAC ÇEK | AAG Lys | GAG Glu | GT3 Val | Leu 70 | TAT Tyr | CAA Gln | CAG Gln | TAC Tyr | GAT Asp 75 | Glu Glu | ATG Met | GAG Glu | gag Glu | 239 |
| TGC Cys 80 | TCG Ser | CAA Gln | GCC Ala | GCC Ala | 923 970 85 | TAC Tyr | ATC Ile | GAA Glu | CAA Gla | GCT Ala 90 | CAG Gln | GTA Val | ATA Ile | GCC Ala | CAC His 95 | 237 |
| CAG Gln | TTC Phe | AAG Lys | Glu | lys 100 | ATC Ile | CTT Leu | GGA Gly | CTG Leu | CTG Leu 105 | CAG Gln | yzā CGY | GCC Ala | acc Thr | CAA Gln 110 | CAA Gln | 335 |
| CAA Gln | GCT Ala | GTC Val | ATT Ile 115 | GAG Glu | Pro | GTA Val | ATA Ile | GCT Ala 120 | TCC Ser | AAC Asn | TIP TIP | CLA Gla | aag Lys 125 | c r. Leu | GAA Glu | 353 |
| | | | | AAG Lys | | | | | | | | | | | | 401 |
| (2) | INF | ORMA: | rion | FOR | SEQ | ID i | 10: 3 | 34: | | | | | | | | |
| | | () E) | 4) La 3) T | ence Engti (PE : OPOL(| : 1: amir | ns Ed | mino cid | | | | | • | | | | |
| | (ii) | MOI | recoi | E T | (7E: | prot | ein | | | | | | | | | |
| | (xi) | SEC | QUENC | E D | ESCR | PTIC | ON: S | SEQ I | D NO |): 3 4 | : : | | | | | |
| Gln 1 | Asn | Glu | Ile | Cys 5 | Leu | Thr | His | Pro | Val 10 | Thr | Lys | Tyr | Ile | Met 15 | Ala | |
| Cys | Met | Ser | Ala 20 | Asp | Leu | Glu | Val | Thr 25 | Thr | Ser | Thr | <u>drb</u> | Val 30 | Leu | Leu | |
| Gly | Gly | Val 35 | Leu | Ala | A <u>i</u> a | Leu | Ala 40 | Ala | Tyr | Суз | Leu | Ser 45 | Val | Gly | Cys | |
| Val | Val 50 | Ile | Val | Gly | His | Ile 55 | Glu | Leu | Gly | Gly | Lys 60 | Pro | Ala | Leu | Val | |
| Pro 65 | Asp | Lys | Glu | Val | Leu 70 | Tyr | Gln | Gln | Tyr | Asp 75 | Glu | Met | Glu | Glu | Cys 80 | |
| Ser | Gln | Ala | Ala | Pro | Tyr | Ile | Glu | Gln | Ala | Gln | Val | Ile | Ala | His | Gln | |

SUBSTITUTE SHEET (RULE 26)

Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln

105

110

Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu Thr 115 120 125

Phe Trp His Lys His

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(Vii) IMMEDIATE SCURCE:

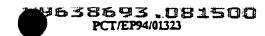
(B) CLONE: BR36-20-164

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

| TC | CAA Gln 1 | AAT Asn | GAA Glu | ATC Ile | TGC Cys 5 | TTG Leu | ACA Thr | CAC His | Pro | ATC Ile 10 | ACA Thr | AAA Lys | TAC Tyt | ATC Ile | ATG Met 15 | 47 |
|------------------|------------------|------------------|------------|------------------|------------------|------------------|------------|------------------|------------------|------------------|------------------|------------------|------------------|------------|------------------|-----|
| GC; Ala | TGC Cys | Mes | TCA Ser | GCT Ala 20 | Asp | CTC Leu | GAN Glu | K GTA Val | ACC Thr 25 | The | : AGC : Sei | ACC Thr | TEE | GIT Val | TTG Leu | 95 |
| CTT | GGA Gly | GGG Gly | GTC Val | Leu | GCG Ala | GCC Ala | CTA Leu | GCG Ala 40 | Ala | TAC Tyr | Cys | TTG Leu | TCA Ser 45 | Val | GGT Gly | 143 |
| TGT Cys | GTT Val | GTG Val 50 | Ile | GTG Val | GGT | CAT His | ATC Ile | Glu | CTG Leu | GGG Gly | GGC Gly | AAG Lys 60 | Pro | GCA Ala | ATC Ile | 191 |
| GTT Val | CCA Pro 65 | Asp | lys | GAG Glu | GTG Val | TTG Leu 70 | Tyr | CAA Gln | CAA Gln | TAC | GAT Asp 75 | Glu | ATG Met | GA: Glu | GAG Glu | 239 |
| TGC Cys 80 | Ser | CAA Gln | GCT Ala | GCC Ala | CCA Pro 85 | TAT Tyr | ATC | GAA Glu | CAA Gln | GCT Ala 90 | Gla | GTA Val | ATA Ile | GCT Ala | CAC His 95 | 237 |
| CAG | TTC | AAG | GGA | AAA | GTC | CTT | GGA | TTG | CTG | CAG | CGA | GCC | ACC | CAP | CAA | 335 |



| Gin Phe Lys Gly Lys Va | al Leu | Gly | Leu | Leu | Gln | Arg | Ala | Thr | Gla | Gln |
|------------------------|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 100 | | | | 105 | | | | | 110 | |

CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG
Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Glm Lys Leu Glu
115 120 125

GCT TTT TGG CAC AAG CAT Ala Phe Trp His Lys His 130

401

- (2) INFORMATION FOR SEQ ID NO: 36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 1 5 10

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Mer Glu Glu Cys 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gin Val Ile Ala His Gln 85 90 95

Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln 100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala 115 120 125

Phe Trp His Lys His

- (2) INFORMATION FOR SEQ ID NO: 37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

| U 9 4 | 1/2560 | 11 | | | | • | | 12 | 6 . | | | | | | PCT | ÆP94 | V 0132 3 |
|--------------|------------------|------------------|----------------------|------------------|----------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------------|----------|-----------------|
| | (ii | .) MC | LECT | ile 1 | YPE: | CDN | A | | | | | | | | | | |
| | (iii | .) ну | ?POT9 | ETIC | AL: | NO | | | | | | | | | | | |
| | (iii | .) An | mı-s | ENSE | : NO | | | | | | | | | | | | |
| | (vii | | MEDI 3) C | | | | 0-16 | 6 | | | | | | | | | |
| | (ix | (| ATUR A) M B) L | AME/ | | | | | | | | | | | | | |
| | (xi |) SE | QUEN | CE D | ESCR | ipti(| ON: : | SEQ . | N CI | 0: 3 ⁻ | 7: | | | | | | |
| rc : | CAA : Gln : | AAT Asn | GAA . Glu | ATC ' | TGC (Cys) | rrg : Leu ' | ACA (Thr : | CAC (His : | CCC . Pro | ATC : Ile : | ACA : | aaa Lys | TAC . Tyr | ATC : | ATG Met 15 | - | 4 |
| ica La | TGC Cys | ATG Mec | TCA Ser | GCT Ala 20 | GAT Asp | CTG Leu | GAA Glu | GTA Val | ACC Thr 25 | ACT Thr | AGC Ser | ACC Thr | TGG TGG | GTT Val 30 | TTG | ; | 9 : |
| TT Leu | GGA Gly | GGG Gly | GTC Val 35 | CTC Leu | GCG Ala | GCC Ala | CTA Leu | GCG Ala 40 | GCC Ala | TAC Tyt | TGC Cys | TTG Leu | TCA Ser 45 | GTC Val | GIY | , | 143 |
| GT Ys | GTT Val | GTG Val 50 | ATT Ile | GTG Val | GGT Gly | CAT His | ATC Ile 55 | GAG Glu | CTG Leu | GGG Gly | GGC Gly | AAG Lys 60 | 523 CCC | GCA Ala | ATC Ile | | 193 |
| TT | CCA Pro 65 | GAC Ç2A | AAA Lys | GAG Glu | GTG Val | TTG Leu 70 | TAT Tyr | CAA Gln | CAA Gln | TAC Tyr | GAT Asp 75 | GAG Glu | ATG Met | GAA Glu | GAG Glu | | 235 |
| GC Vs | TCA Ser | CAA Glr | GCT | GCC | CCA | TAT | ATC | GAA | CZA G) = | GCT | CAG | GTG | ATA | GCT | CAC | | 287 |

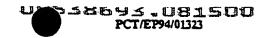
CAG TTC AAG GAA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln 100 CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG 383 Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu

115 125 . GCC TTT TGG CAC AAG CAT 431 Ala Phe Trp His Lys His

(2) INFORMATION FOR SEQ ID NO: 38:

130

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 133 amine acids



- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala 1 5 10

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln 85 90 95

Phe Lys Glu Lys Val Leu Gly Leu Leu Gin Arg Ala Thr Gin Gin Gin 100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala 115 120 125

Phe Trp His Lys His

- (2) INFORMATION FOR SEQ ID NO: 39:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-20-165

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 3..401
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

| | 1 | ASN | GAA Glu | IIE | Cys 5 | Leu | Thr | His | Pro | Ile 10 | Thr | Lys | TYT | Ile | Met 15 | 47 |
|------------------|------------------|------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|--------------------|------------------|-------|
| ~~a | . Cys | mes | . ser | 20 | Asp | Leu | Glu | . Val | 7h= 25 | Thr | Ser | Thr | فتي | Val 30 | | 95 |
| CTT Leu | GGA Gly | GGG Gly | GTC Val 35 | Leu | GC3 Ala | GCC Ala | CTA Leu | GCG Ala 40 | GCC Ala | TAC | TGC | TTG Leu | TCA Ser 45 | GTC Val | GGT Gly | 143 |
| TGT Cys | GTT Val | GTG Val 50 | ATT | GTG Val | GGT Gly | CAT His | ATC Ile 55 | GAG Glu | CTG Leu | GGG Gly | GGC | AAG Lys 60 | CCG | GCA Ala | ATC Ile | 191 |
| GTT Val | CCA Pro 65 | GAC Asp | AAA Lys | GJ n | GTG Val | TTG Leu 70 | TAT Tyr | CAA Gl:: | CAĄ Gln | TAC Tyr | GAT Asp 75 | GAG Glu | ATG Met | GAA Glu | GAG Glu | . 239 |
| TGC Cys 80 | TCA Ser | CAA Gln | GCT Ala | GCC Ala | CCA Pro- 85 | TAT Tyr | ATC Ile | GAA Glu | CAA Glm | GCT Ala 90 | CAG Gla | GTA Val | ATA Ile | GCT Ala | CAC His 95 | 297 |
| CAG Gim | TTC Phe | AAG Lys | GAA Glu | AAA Lys 100 | GTC Val | CTT Leu | GGA Gly | TTG Leu | CTG Leu 105 | CAG Gln | Arg CGA | GCC Ala | ACC Thr | CAA Gl:: 110 | CAA Gla | 335 |
| CAA Gin | GCT Ala | GTC Val | ATT Ile 115 | GAG Glu | CCC Pro | ATA Ile | GTA Val | ACT Thr 120 | ACC Thr | AAC Asa | TTP TGG | CAA Glm | AAG Lys 125 | CTT Leu | GAG Glu | 383 |
| GCC Ala | | | | | | | | | | | | | | | | -401 |

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Mer Ala

1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys 35 40 45

| Va! | Val 50 | Ile | Val | Gly | His | Ile 55 | Glu | Leu | Gly | Gly | Lys 60 | Pro | Ala | Ile | Val |
|-----------|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|
| Pro 65 | Asp | | | Val | | T): | Gln | Gln | Tyr | Asp | Glu | Mec | Glu | Glu | Суз |

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln 85 90 95

Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln 100 . 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala 115 120 125

Phe Trp His Lys His

(2) INFORMATION FOR SEQ ID NO: 41:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleis acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: limear
- (ii) MOLECULE TYPE: cDNA
- (iii) EYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE: (B) CLONE: PC-2-1
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 (B) LOCATION: 3..509
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:
- CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC

 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr

 1 5 10 15

 AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT

 Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val
- GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC

 143
 Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg

 35
- GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG 191 Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln

239

50

CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro

55

65 70

GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG 287 Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly 85

TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC 335 Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp 100

CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG 383 Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr 115

TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC 431 Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro 130

ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG 479 Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu 145

GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA 509 Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu 160

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 amino acids
 - (B) TYPE: amino acid
 - (D) TOPCLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 55

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp

90 95

| Leu | Leu | Ser | Pro | Arg | CJÀ. | Ser | Arg | Pro | Asn | Trp | Gly | Pro | Asn | Asp | Pro |
|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | | | 100 | | | | | 105 | | • | | | 110 | | |

Arg Arg Lys Ser Arg Asm Leu Gly Lys Val Ile Asp Thr Leu Thr Cys

Gly Phe Ala Asp Leu Met Gly Tyr Île Pro Leu Val Gly Gly Pro Ile 130 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 145 150 155 160

Gly Val Asn Tyr Ala Thr Gly Asn Leu 165

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cona
- (iii) HYPOTHETICAL: NO
- (111) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE: (B) CLONE: PC-2-6
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 3..509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

| CC ATO | AGC | ACG | AAT | CCT | $\lambda\lambda\lambda$ | CCT | CAA | AGA | AAA | ACC | AAA | AGA | AAC | ACC | 47 |
|--------|-----|-----|-----|-----|-------------------------|-----|-----|-----|-----|-----|-----|------|-----|-----|----|
| Met | Ser | Thr | asa | Pro | Lys | Pro | Gln | Arg | Lys | Thr | Lys | Arg. | Asn | Thr | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

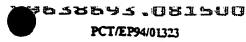
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT

Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val

20
25
30

GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC 143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg
45

GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG 191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln
50



| ,,, | | *1 | | | | • | | 1: | 32 | | | | , | | PCT/E | P94/01 | 323 |
|-------------------|-------------------|-------------------|-------------------------|-----------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|------------------|--------|------|
| Pro | ATT Ile 65 | ALO | AAG Lys | GCG Ala | Arg | CAG Gla 70 | Sic | ACG Thr | GGC Gly | CGG Arg | TCC Ser 75 | dıı | GGT Gly | CAA Gln | CCC Pro | | 239 |
| GGG Gly ao | TAC | Pro | ITP | CCC Pro | CTT Leu 85 | TAC Tyr | GCC Ala | AAT Asn | GAG Glu | GGC Gly 90 | CIC | GGG Gly | TGG Trp | GCA Ala | GGG Gly 95 | | 287 |
| irb iec | CTG Leu | CTC | TCC | CCT PTO 100 | YZ. CGY | GGC Gly | TCT Ser | CGG ATG | CCT Pro 105 | AAT Asn | TGG Tap | GGC | B10 CCC | AAT Asn 110 | GAC ÇeA | | 335 |
| Pro CCC | CGG Arg | CGA | AAA Lys 115 | TCG Ser | CGT Arg | TAA Asn | TTG Leu | GGT Gly 130 | AAG Lys | GTC Val | ATC Ile | GAT Asp | ACC Thr 125 | CTA Leu | ACG Thr | | .383 |
| TGC Cys | GGA Gly | TTC Phe 130 | GCC ['] Ala | GAT Xsp | CTC Leu | ATG Mes | GGG Gly 135 | TAT Tyr | ATC Ile | CCG Pro | CTC Leu | GTA Val 140 | GGC Gly | GGC Gly | CCC Pro | | 431 |
| ATT | GGG Gly 145 | GGC Gly | GTC Val | GCA Ala | AGG Arg | GCT Ala 150 | CTC | GCA Ala | CAC His | GGT Gly | GTG Vai 153 | AGG Azg | GTC Val | CTT Leu | GAG Glu | | 479. |
| GAC Asp 160 | GGG Gly | GTA Val | AAC Asn | TAT Tyr | GCA Ala 165 | ACA Thr | G17 GGG | AAT Asn | TTA Leu | | | | | | | • | 509 |
| (2) | INFO | RMAT | ION | FOR | SEQ | ID N | O: 4 | 4: | | | | | | | | | |
| | (| K) E) |) LE | nce Digth Pe: Polo | : 16 amin | 9 am | ino id | | | | | | | | | | |
| | (ii) | MOL | ECUL | E TY | PE: | pret | ein | | | | | | | | | | |
| | (xi) | SEQ | UENC | E DE | SCRI | PTIC | N: S | EQ I | סא פ | : 44 | : | | | | | | |
| Met 1 | Ser | Thr | Asn | Pro 5 | Lys | Pro | Gln | Arg | Lys 10 | Thr | Lys | Arg | Asn | Thr 15 | Asn | | |
| Arg | Arg | Pro | Gln | Asp | Val | I.ve | מלם | Dra | 611/ | C) v | G1 | <i>-</i> 1- | 7 3.0 | **- 3 | 61 | | |

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35 40

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp 85 90



| VO 94 | /2560 |)1 | | | | • | | . 1 | 33 | | | | | 523 | PCTÆ | P94/01 | ප 323 |
|--------------|------------|----------------|-------------------------|----------------------|-----------------------|------------------------------------|----------------------|----------------|-------------------|----------------|--------------|--------------|------------|-------------------|------------|--------|----------|
| Leu | Leu | Ser | Pro 100 | Arg | Glγ | Ser | Arg | Pro 105 | Asn |) Tzp | Gly | Pro | Asn 110 | Ąsp | Pro | | |
| Arg | Arg | Lys 115 | Ser | Arg | Asn | Leu | Gly 120 | Lys | Val | Ile | Asp | Thr 125 | Leu | Thr | Cys | | |
| Gly | Phe 130 | λla | Ąsp | Leu | Met | Gly 135 | Tys | Ile | Pro | Leu | Vai 140 | Gly | Gly | Pro | Ile | | |
| Gly 145 | Gly | Val | Ala | Yzâ | Ala 150 | Leu | AL'a | His | Gly | Val 155 | کتع | Val | Leu | Glu | Asp 160 | | |
| Gly | Val | Asn | Tyr | Ala 165 | Thr | Gīy | Aşn | Leu | | | | | | | | | |
| (2) | INFO | RMAT | 'ION | FOR | SEQ | ID N | TO: 4 | 15: | | | | | | | | | |
| | (1) | 4) 2) () | l) LE I) TY I) ST | ngte Pe : Rant | 1: 58 חשכו באכם | TERI 0 ba eis SS: line | se p acid sing | airs I | ; | | | | | | | - | |
| | (ii) | MOL | ECUL | Z TY | PE: | cDNA | | | | | | | | | | | |
| (: | iii) | HYP | OTHE | TIC | I: N | o o | | | | | | | | | | | |
| (: | iii) | ANT | I-SE | NSE: | NO | | | | | | | | | | | | |
| (1 | /ii) | | | TE S CNE: | | | | | | | | | | | | | |
| , | (ix) | (A | | ME/X | | CDS 25 | 80 | | | | | | | | | | |
| 1 | (xi) | SEQ | UENC | E DE | SCRI | PTIO | N: S | EQ I | D NO | : 45 | : | | | | | | |
| A ACC Thi | Cy | C GG S G1 | A TTO | C GC e Al | C GA a As 5 | T CT | C AT | G GG c Gl | G TA Y TY 1 | = Il | C CC e Pr | G CT o Le | C GT | l Gl | Y S | | 46 |
| GGC C | ro : | ATT (| GGG (| GGC Gly 20 | GTC Val | GCA . Ala : | AGG Arg | GCT Ala : | CTC (Leu ; | GCA (Ala : | CAC His | GGT (| GTG Val | AGG Arg 30. | Val | | 94 |
| TT G | AG (| SAC (| GGG (| GTA : | AAC | TAT (| GCA . | ACA (| GGG / | AAT ' | TTA | CCC (| GGT | TGC | TCT . | : | 14: |

| A ACG TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly 1 5 10 15 | 46 |
|--|-----|
| GGC CCC ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC Gly Pro Ile Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val 25 . 30 | 94 |
| CTT GAG GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser 35 40 45 | 142 |
| TTC TCT ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC Phe Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala 50 55 60 | 190 |
| TCT GCA GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT | 238 |

| Ser | Ala 65 | Val | Pro | Tyr | Arg | Asn 70 | Ala | Ser | Gly | Ile | Tyr 75 | His | Val | Thr | Asn | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| GAT Asp 80 | Cys | CCA Pro | AAC Asn | TCT Ser | TCC Ser 85 | ATA Ile | GTC Val | TAT Tyr | GAG Glu | GCA Ala 90 | TAÐ qeA | AAC Asa | CTG Leu | ATC Ile | CTA Leu 95 | 286 |
| CAC Sik | GCA Ala | CCT | GGT Gly | TGC Cys 100 | GTG Val | CCT Pro | TGT Cys | GTC Val | ATG Met 105 | ACA Thr | GGT Gly | AAT Asn | GTG Val | AGT Ser 110 | AGA Azg | 334 |
| TGC Cys | TCG | GTC Val | CAA Gln 115 | ATT Ile | ACC Thr | CCT Pro | ACA Thr | CTS Leu 120 | TCA Ser | GCC Ala | Pro | AGC Ser | CTC Leu 125 | gga Gly | GCA Ala | 382 |
| GTC Val | ACG Thr | GCT Ala 130 | CCT Pro | CTT Leu | CGG Arg | AGA Arg | GCC Ala 135 | GTT Val | GAC Asp | TAC Tyr | CTA Leu | GCG Ala 140 | GGA Gly | GGG Gly | GCT Ala | 430 |
| GCC Ala | CTC Leu 145 | TGC Cys | TCC Ser | GCG Ala | TTA Leu | TAC Tyr 150 | GTA Val | GGA Gly | GAC Asp | GCG Ala | TGT Cys 155 | GGG Gly | GCA Ala | CTA Leu | TTC Phe | 478 |
| TTG Leu 160 | GTA Val | GGC Gly | CAA Gln | ATG Met | TTC Phe 165 | ACC Thr | TAT Tyr | agg Azg | Sis | CGC Arg 170 | CAG Gln | CAC His | GCT Ala | ACG Thr | GTG Val 175 | 526 |
| CAG Gln | AAC Asn | TGC Cys | AAC Asn | TGT Cys 180 | TCC Ser | ATT Ile | TAC Tyr | AGT Ser | GGC Gly 185 | CAT Els | GTT Val | ACC Thr | GGC Gly | CAC His 190 | CGG Arg | 574 |
| ATG Met | | | | | | | | | | | | | | | | 580 |

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10

Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 30

Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60



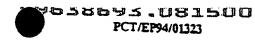
135 Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pr Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Ash Val Ser Arg Cys Try Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu 145 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln 170 Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met 180 Ala (2) INFORMATION FOR SEQ ID NO: 47: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 580 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single . (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA (iii) HYPOTHETICAL: NO (iii) ANTI-SENSE: NO (vii) IMMEDIATE SOURCE: (B) CLONE: PC-4-6 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 2..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

A ACG TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly 1 5

94

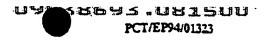
GGC CCC ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC



| G1 | y Pr | o Il | e Gly | (Gl ₃ | / Val | . Ala | . Arg | , Ala | a Let | د مند د | a Sig | Gl _y | / Val | L Arg | ; Val | |
|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------------|-------------------|----------------------|-------------------|-------------------|-----|
| CT: Let | r ga u gl | GA(L Asp | GG G1 y | | AAC Asn | TAI | GCA Ala | ACA Thr | GI | AA: Asi | TTA Lev | SEC | GG1 Gly | Cys | TCT Ser | 14. |
| TT: Phe | C TCT | T ATO | | ATT | CTT | GCT Ala | CTT Leu 55 | Leu | : TCG : Ser | Cha 131 | CTS Leu | ACC Thr | Val | CCG Pro | GCC Ala | 190 |
| TCT Ser | GCA Ala 65 | 101 | Pro | TAC Tyr | CGA Arg | AAT Asn 70 | GCC Ala | Ser | G1y | ATT Ile | TAT Tyr 75 | CAT His | G Val | ACC Thr | AAT Ásn | 238 |
| GAT Asp 80 | -13 | CCA PTO | AAC Asn | TCT Ser | TCC Ser 85 | ATA Ile | GTC Val | TAT Tyr | GAG Glu | GCA Ala 90 | λsp | AAC Ast | CTG Leu | ATC Ile | CTA Leu 95 | 286 |
| CAC His | GCA Ala | Sio | GGT Gly | TGC Cys 100 | GTG Val | CCT Pro | TGT Cys | GTC Val | ATG Mes 105 | ACA Thr | GGT Gly | AAT Ast | GTG Val | AGT Ser | AGA Arg | 334 |
| TGC Cys | ICC TCC | GTC Val | CAA Glm 115 | ATT Ile | ACC Thr | CCT Pro | ACA Thr | CTG Leu 120 | TCA Ser | GCC Ala | CC3 | AGC Ser | CTC Leu 125 | GGA Gly | GCA Ala | 382 |
| GTC Val | ACG Thr | GCT Ala 130 | CCT Pro | CTI Leu | CGG Arg | AGA Azg | GCC Ala 135 | GTT Val | وجر درعد | TAC Tyr | CTA Le u | GCG Ala 140 | | GGG Gly | GCT Ala | 430 |
| GCC Ala | CTC Leu 145 | TGC Cys | TCC Ser | GCG Ala | Let | TAC Tyr 150 | GTA Val | GGA Gly | GAC Asp | GCG Ala | TGT Cys 155 | | GCA Ala | CTA Leu | TTC Phe | 478 |
| TTG Leu 160 | GTA Val | GGC Gly | CAA Gln | wec | TTC . Phe 1 | acc Thr | TAT Tyr | AGG Arg | 220 | CGC Arg 170 | CAG Glm | CAC His | GCT Ala | ACG Thr | GTG Val 175 | 525 |
| CAG Gln | AAC Asn | TGC Cys | ASA | TGT Cys 180 | TCC : | ATT | TAC . | Ser | GGC Gly 185 | CAT Eis | GTT Val | ACC Thr | Gly | CAC His 190 | CGG | 574 |
| ATG Met . | | | | | • | | | | | | | | | | | 580 |

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear -
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:



Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly

1 5 10 15

Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 30

Glu Asp Gly Val Ash Tyr Ala Thr Gly Ash Leu Pro Gly Cys Ser Phe 35 40

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His
85 90 95

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys 100 105 110

Trp Val Gin Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Giy Ala Val 115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu 145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln 165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met 180 195 190

Ala

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 (B) CLONE: PC-3-4

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 3..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

| | 1 | | | | _ | | 720 | GIH | Arg | Lys 10 | Thr | Lys | λι | , As: | Thr 15 | 47 |
|------------------|-------------------|--------------|-------------------|-------------------|----------------------|-------------------|-------------------|-----------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| | | | • | | 20 | , va. | L Ly: | s Pre | 23 | 2 2 GT | Y Gl | y Gl | y Gl | n Il 3 | - | 95 |
| | | • | : | 35 | | | ، مدو | 40 |) GT} | , PIC |) Arg | ; Me | = G1 4 | y Va. 5 | G CGC L Arg | 143 |
| | | 5 | Ö . | | | . 0 | 55 | 3e: | GIN | PTO | Arg | G1; | / Ar: | 3 Yz | F CAG Gln | 191 |
| CCT Pro | ATT Ile 65 | CC Pr | C AA o Ly | G GC 's Ai | G CGC a Arg | CAG Gln 70 | Pro CCC | ACG Thr | GGC Gly | Cತ್ತೆ ನಿಶ್ವ | TCC Ser 75 | T | GG: Gly | CA Gl: | CCC Pro | 239 |
| GGG Gly 80 | TAC Tyr | St. | T TG | G CC P Pr | C CTT O Leu 85 | -11- | GCC Ala | AAT Asn | GAG Glu | GGC Gly 90 | CTC Leu | GGG Gly | TTG | G GCX Ala | GGG Gly 95 | 297 |
| 1.tb | CTG Leu | CTC | I TC | C CC T Pro | T CGA D Arg D | GGC Gly | TCT Ser | CGG Arg | CCT Pro 105 | AAT Asn | Trp | GGC Gly | . 5 20 | AAT Asn 110 | GAC G2A | 335 |
| CCC | CGG Azg | CG; Arg | Ly: | | G CGT F Arg | AAT Asn | TTG Leu | GGT Gly 120 | AAG Lys | GTC Val | ATC Ile | GAT Asp | ACC Thr 125 | Leu | ACG Thr | 383 |
| TGC (| GGA Gly | Phe | GCC Ala | GAT Asp | CTC Leu | ATG Met | GGG Gly 135 | TAT Tyr | ATC Ile | CCG Pro | CTC Leu | GTA Val 140 | GGC Gly | GGC Gly | CCC Pro | 431 |
| ATT (| 3G3 31y 145 | GGC Gly | GTC Val | GCA Ala | AGG | GCT Ala 150 | CTC Leu | GCA Ala | CAC His | Gly ' | GTG Val 155 | AGG Arg | GTC Val | CTT Leu | GAG Glu | 479 |
| GAC 0 Asp 0 | GG Gly | GTA Val | AAC Asn | TAT | GCA Ala 165 | ACA (Thr (| GGG . Gly . | AAT ' Asn : | Leu : | CCC (Pro (| GGT Gly | TGC Cys | TCT Ser | TTC Phe | TCT Ser 175 | 527 |
| ATC T | TT ; | ATT Ile | CTT Leu | GCT Ala 180 | CTT Leu | CTC : | rcg : Ser (| .ys 1 | CTG / Leu 1 | 900 (Thr 1 | GTT (Val) | ccg Pro | GCC Ala | TCT Ser 190 | GCA Ala | 575 |
| GTT C | cc 1 | rac ryr ' | CGA Arg 195 | AAT Asn | GCC 1 | TCT (| TY I | ATT 1 Lie 1 200 | rat c Pyr e | CAT C | FTT 2 /al 1 | רהד | AAT Asn 205 | GAT Asp | TGC | 623 |
| | | | | | | | | | | | | | | | | |



| | CCA | AAC | TCT | TCC | ATA | GTC | TAT | GAG | GCA | GAT | AAC | CTG | ATC | CTA | CAC | GCA | | 671 |
|-----------|-----|------|-------|----------------|------------|------|------|--------|------|------|-------|---------------------|------|-----|------------|-----|---|-----|
| | Pro | Asn | Ser | Ser | Ile | Val | Ty | Glu | Ala | Asp | Asn | Leu | Ile | Leu | His | Ala | | |
| | | | 210 | | | | | 215 | | | | | 220 | | | | | |
| | CCT | GGT | TGC | GTG | CCT | TGT | GTC | ATG | ACA | GGT | 227 | GTG | AGT | AG2 | TGC | TGG | | 719 |
| | Pro | Gly | Cys | Val | 22 | Cys | Val | Met | Thr | Gly | Asn | Vai | Ser | Arg | Cys | Tro | | 163 |
| | • | 225 | | | | | 230 | | | • | | 235 | | _ | • | • | | |
| <u>``</u> | منت | ~~~ | 8 700 | | | 3.03 | ~~~ | | | | | | | | | | | |
| | | | | ACC Thr | | | | | | | | | | | | | | 767 |
| | 240 | | | | | 245 | | | ~ | | 250 | Deu | GLŸ | ATG | ATT | 255 | | |
| | | | | | | | | | | | | | | | | | | |
| | | | | CGG | | | | | | | | | | | | | | 815 |
| | Ala | PIO | Leu | yrg | AFG 260 | Ala | val | qzA | Tyr | 265 | Ala | Glà | Gly | Ala | Ala 270 | Leu | | |
| | | | | | | | | | | 203 | | | | | 270 | | | |
| | | | | TTA | | | | | | | | | | | | | | 863 |
| | Cys | Ser | Ala | Leu | Tyr | Vai | Gly | ģek | | Cys | Gly | Ala | Leu | | Leu | Val | | |
| | | | | 275 | | | | | 290 | | | | | 285 | | | | |
| | GGC | CAA | ATG | TTC | ACC | TAT | AGG | CCI | CGC | CAG | CAC | GCT | ACG | GTG | CAG | AAC | | 911 |
| | | | | Phe | | | | | | | | | | | | | | |
| | | | 290 | | | | | 295 | | | | | 300 | | | | | |
| | TGC | ASC | TCT | - | 3 | 72.7 | ac= | GGC | C3. | ست | 300 | 000 | as a | ~~~ | x === | GCA | • | 000 |
| | Cys | Asn | Cys | Ser | Ile | Tyr | Ser | Gly | His | Val | Thr | G17 | nis | Are | Met | Ala | | 959 |
| | • | 305 | • | | | • | 310 | • | | | | 315 | | | | | | |
| | | | | | | | | | | | | | | | | | | |
| | (2) | INFO | PMAT | IGN | ±0.5 | 550 | א מז | io - s | ia. | | | | | | | | | |
| | , | | | | | J_4 | | | | | | | | | | | | |
| | | (| | EQUE | | | | | | | | | | | | | | |
| | | | | LE | | | | | acid | !s | | | | | | | | |
| | | | | 3) TY 3) TO | | | | | | | | | | | | | | |
| | | | | , | | ••• | | | | | | | | | | | | |
| | | (ii) | MOL | ECIL | E TY | PE: | prot | ein | | | | | | | | | | |
| | | (xi) | SEC | UENC | E DE | SCRI | PTIC | N: S | EQ 1 | D NO |): 50 |): | | | | | | |
| | Met | Ser | Thr | Asn | Pro | Lvs | Pro | Gln | Arc | Lvs | Thr | Lvs | Aro | Asp | The | Asn | | |
| | 1 | | | | 5 | _, _ | | | 3 | 10 | J | - , - | | | 15 | | | |
| | Ara | Ara | Pro | Gla | 2 = ~ | Va: | T.VS | Phe | P=3 | GIV | Gly | 61.2 | Gla | Tla | 17=1 | Gly | | |

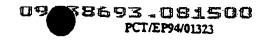
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35 40

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg-Ser Trp Gly Gln Pro Gly
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Ala Asa Glu Gly Leu Gly Trp Ala Gly Trp 85 90 95



- Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
- Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
- Gly Phe Ala Asp Leu Met Gly Tyr Tle Pro Leu Val Gly Gly Pro Ile 130 140
- Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 145 150 155 160
- Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 165 170 175
- Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
- Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro 195 200 205
- Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro 210 215 220
- Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val 225 230 235 240
- Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala 245 250 255
- Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys 265 270
- Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly 275 280 235
- Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys 290 295 300
- Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala 305 310 315
- (2) INFORMATION FOR SEQ ID NO: 51:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:



(B) CLONE: PC-3-8

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 3..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

| cc | ATG | acc. | 203 | 227 | سبم | 233 | | er s | AGA | ••• | 300 | ••• | | | | |
|-------------------|-----------|------------|-------|------------|--------------|--------------|--------------------|-----------|----------|------------|------------|-------------|------------|------------|------------|-----|
| - | Met | Ser | Thr | Asn | Sio | Lys | Pro | Glm | Arg | Lys | Thr | Lys | Ara | Asn | ACC Thr | 47 |
| | 1 | | | | 5 | | , | • | | 10 | | -•- | 3 | | 15 | |
| AAC | CG1 | . cec | : cc | دمد | GAC | GTC | AAG | TTC | CCG | GGC | : GG: | GGT | CAG | ATC | GTT | 95 |
| Asn | Arg | Arg | Pro | 20 20 | | Val | Lys | Phe | 25 | | r Gly | r Gly | / Gln | Ile 30 | | |
| GGC | GGA | GTT | TAC | TTG | TTG | CCG | cso | AGG | GGC | CCI | AGG | ATG | GGT | GTG | CGC. | 143 |
| ĠŦÅ | . GTÅ | va: | 35 | | Leu | Pro | Arg | Arg 40 | | Pro | . Arg | Met | Gly 45 | | Arg | • |
| GCG | ACT | CGG | AAG | ACT | TCG | GAA | CGG | TCG | CAA | ccc | CGT | GGA | CGG | CGT | CAG | 191 |
| Ala | Thr | Arg 50 | | Thr | Se: | Glu | λ r g 55 | | . Glu | Pro | Arg | 61y | | Arg | Gln | |
| CCT | ATT | CCC | AAG | GCG | CGC | CAG | CCC | ACG | GGC | CGG | TCC | TGG | GGT | CAA | CCC | 239 |
| Pro | Ile 65 | | Lys | Αla | . Arg | Gin 70 | | The | Gly | Arg | 5e: 73 | | Gly | Gln | Pro | |
| GGG | TAC | CCI | TGG | ccc | CIT | TAC | GCC | AAT | GAG | GGC | CTC | GGG | TGG | GCA | GGG | 257 |
| GLY 80 | | Pro | ım | Pro | . Leu 185 | | Ala | As: | Glu | Gly | | Gly | . Irb | Aia | Gly | |
| | | | | | | | | | | | | | | | 95 | |
| TGG | CTG | CTC | TCC | CCI | CGA | GGC | TCT | CGG | CCT | AAT | TGG | GGC | CCC | AAT | GAC | 335 |
| *** | sed | red | . ser | 100 | | GIV | Ser | , YL. | 105 | ASD | ızb | etň | , bio | 110 | çeA | |
| | | | | | | | | | | | | | | | ACG | 383 |
| hio | Arg | Arg | 115 | | Arg | Asn | Leu | 120 | Lys | Val | Ile | çe <i>k</i> | Thr 125 | | Thr | |
| | | | | | | | | | | | | | | | CCC | 431 |
| Cys | GTA | Phe 130 | | Asp | Leu | Mes | Gly 135 | | Ile | Pro | Leu | Val 140 | _ | Gly | Pro | |
| | | | | | | | | | | | | | | | GAG | 479 |
| Val | 145 | | Val | Ala | Yzg | . Ala 150 | | . Ala | His | Gly | Val 155 | - | Val | Leu | Glu | |
| | | | | | | | | | | | | | | | TCT | 527 |
| Asp 160 | Gly | Val | Asn | ŢŸï | Pro 165 | | Gly | Asn | Leu | Pro 170 | | Cys | Ser | Phe | Ser 175 | |
| ATC | TIT | ATT | CTT | GCT | CTT | CTC | TCG | -IG: | CTG | ACC | GTT | ccc | GCC | TCT | GCA | 575 |
| Ile | Phe | Ile | Leu | Ala 180 | | Leu | Ser | Cys | 162 7 | Thr | Val | Pro | Ala | Ser 190 | Ala | |
| GTT | ccc | TAC | CGA | AAT | GCC | TCT | GGG | ATT | TAT | CAT | GTT | ACC | . AAT | GAT | TGC | 623 |

| Va) | Pro | Tyr | A r g 195 | λsn | Ala | Ser | Gly | Ile 200 | | His | Val | Thr | Asn 205 | Asp | Cys | |
|-------------------|-------------------|-------------------|---------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|---------|
| Pro | AAC Asn | TCT Ser 210 | TCC | ATA Ile | GTC Val | TAT Tyr | GAG Glu 215 | GCA Ala | GAT Asp | AAC Asn | CTG Leu | ATC Ile 220 | CTA Leu | CAC His | GCA Ala | 671 |
| Pro | GGT Gly 225 | TGC Cys | GTG Val | CCT Pro | IGT Cys | GTC Val 230 | ATG Mes | ACA Thr | GGT Gly | aat Asi | GTG Val 235 | AGT Ser | ACA | TGC Cys | TGG Trp | 719 |
| GTC Val 240 | CAA Gln | ATT Ile | ACC Thr | CCT Pro | ACA Thr 245 | CTG Leu | TCA Ser | GCC Ala | CCG Pro | AGC Ser 250 | CTC Leu | GGA Gly | GCA Ala | GTC Val | ACG Thr 255 | 767 |
| GCT Ala | Pro | CTT | CGG Arg | AGA Arg 260 | GCC Ala | GTT Val | GAC Asp | TAC Tyr | CTA Leu 265 | GCG Ala | GGA Gly | GGG Gly | GCT Ala | GCC Ala 270 | CTC Leu | 815 |
| TGC Cys | TCC Ser | Ala | TTA Leu 275 | TAC Tyr | GTA Val | GGA Gly | GAC Asp | GCG Ala 280 | TGT Cys | GGG Gly | GCA Ala | CTA CTA | TTC Phe 285 | TTG Leu | GTA Val | 863 |
| G1. | CAA Gla | ATG Met 290 | TTC Phe | ACC Thr | TAT Tyr | YL3 YCG | CCT 295 | CGC | CAG Gln | CAC His | GCT Ala | ACG Thr 300 | GTG Val | CAG Gln | AAC Asn | 911 |
| Càa | AAC Asn 305 | TGT Cys | TCC Ser | ATT Ile | TAC Tyr | AGT Ser 310 | GGC | CAT Kis | GTT Val | ACC Thr | GGC Gly 315 | CAC | CGG | ATG Met | GCA Ala | 959 |
| (2) | TNEC | ous.m | TAN | 207 | | . | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

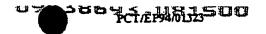
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro

Ile Pro Lys Ala Arg Glm Pro Thr Gly Arg Ser Trp Gly Glm Pro Gly 65 70 75 80



Tyr Pro Trp Pro Leu Tyr Ala Asa Glu Gly Leu Gly Trp Ala Gly Trp 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asm Trp Gly Pro Asm Asp Pro

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys 115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val 130 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 145 150 153 160

Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 165 170 175

Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val 180 185 190

Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro 195 200 205

Ash Ser Ser Ile Val Tyr Glu Ala Asp Ash Leu Ile Leu His Ala Pro 210 215 220

Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val 225 230 235 240

Gin The Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala

Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys 260 265 270

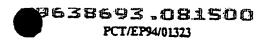
Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly 275 280 285

Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys

Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala 305 310 315

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 959 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO



(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC C/E1

(ix) PEATURE:

- (A) NAME/NEY: CES
- (B) LOCATION: 2..959

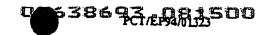
(xi) SEQUENCE DESCRIPTION: SEQ ID MC: 53:

| CCATGAGCAC | : GAATCCTAAA | CETERARGAR | AAACCAAAAG | AAACACCAAC | CGTCGCCCAC | 60 |
|------------|--------------|------------|------------|------------|--------------|-----|
| AGGACGTCA | GTTCCCGGGC | GGTGGTCAGA | TCGTTGGCGG | AGTTTACTTG | TTGCCGCGCA | 120 |
| GGGGCCCTAG | GATGGGTGTG | CGCGCGACTC | GGAAGACTTC | GGAACGGTCG | CAACCCCGTG - | 130 |
| GACGGCGTCA | GCCTATTCCC | AAGGCGCGCC | AGCCCACGGG | CCGGTCCTGG | GGTCAACCCG | 240 |
| GGTACCCTTG | GCCCCTTTAC | GCCAATGAGG | GCCTCTGGTG | GGCAGGGTGG | CTGCTCTCCC | 300 |
| CTCGAGGCTC | TCGGCCTAAT | TGGGGCCCCA | ATGACTCCCG | GCGAAAATCG | CSTAATTTGG | 350 |
| GTAAGGTCAT | CGATACCCTA | ACGTGCGGAT | TOGOCCATOT | CATGGGGTAY | ATCCCGCTCG | 420 |
| TAGGCGGCCC | CRTTGGGGGC | GTCGCAAGGG | CTCTCGCACA | CGGTGTGAGG | GTCCTTGAGG | 480 |
| ACGGGGTAAA | CTATSCAACA | GGGAATTTAC | CCGGTTGCTC | TTTCTCTATC | TTTATTCTTG | 540 |
| CTCTTCTCTC | GTGTCTGACC | GTTCCGGCCT | CTGCAGTTCC | CTACCGAAAT | GCCTCTGGGA | 600 |
| TTTATCATGT | TACCAATGAT | TGCCCAAACT | CTTCCATAGT | CTATGAGGCA | GATAACCTGA | 650 |
| TCCTACACGC | ACCTGGTTGC | GTGCCTTGTS | TCATGACAGG | TAATGTGAGT | AGATGCTGGG | 720 |
| TCCAAATTAC | CCCTACACTG | TCAGCCCCGA | GCCTCGGAGC | AGTCACGGCT | CCTCTTCGGA | 780 |
| GAGCCGTTGA | CTACCTAGCG | GGAGGGGCTG | CCCTCTGCTC | CGCGTTATAC | GTAGGAGACG | 840 |
| CGTGTGGGGC | ACTATTCTTG | GTAGGCCAAA | TGTTCACCTA | TAGGCCTCGC | CAGCACGCTA | 900 |
| CGGTGCAGAA | CTGCAACTGT | TOCATTIACA | GTGGCCATGT | TACCGGCCAC | CGGATGGCA | 959 |
| | | | | | | |

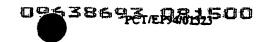
(2) INFORMATION FOR SEQ ID NO: 54:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15



- Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 25 30
- Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35 40 45
- Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
- Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly 65 70 75 80
- Tyr Pro Trp Pro Leu Tyr Ala Asm Glu Gly Leu Gly Trp Ala Gly Trp 85 90 95
- Leu Leu Ser Pro Arg Gly Ser Arg Pro Asa Trp Gly Pro Asa Asp Pro
- Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
- Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val 130 135 140
- Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 150 155 160
- Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 165 170 175
- Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val
- Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro 195 200 205
- Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro 210 215 220
- Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val 225 230 235 240
- Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala 245 250 255
- Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys
 260 265 270
- Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly 275 280 285
- Gln Mec Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys 290 295 300
- Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala 305 310 315



| (2) | INFORMATION | FCR S | מו כא | NO - | 55. |
|-----|-------------|-------|-------|------|-----|
| | | | | | |

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) EYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:

(B) CLONE: PC-1-37

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..354
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

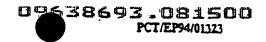
| ACCACCGGAG | CTTCTATCAC | ATACTECACT | TACGGCAAGT | TCCTTGCTGA | TGGAGGGTGT | 60 |
|------------|------------|------------|------------|------------|------------|-----|
| TCAGGCGGCG | CGCATGACGT | GATCATATGC | GACGAGTGCC | ATTCCCAGGA | CGCCACCACC | 120 |
| ATTCTTGGGA | TAGGCACTGT | CCTTGACCAG | GCAGAGACGG | CTGGAGCTAG | GCTCGTCGTC | 190 |
| TTGGCCACGG | NCACCCCTCC | CGGCAGTGTG | ACAACGCCCC | ACCCCAACAT | CGAGGAAGTG | 240 |
| GCCCTGCCTC | AGGAGGGGGA | GGTTCCCTTC | TACGGCAGAG | CCATTCCCCT | TGCTTTTATA | 300 |
| AAGGGTGGTA | GGCATCTCAT | CTTCTGCCAT | TCCAAGAAAA | ATTGTGATGA | ACTC | 354 |

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala 1 5 10

Asp Gly Gly Cys Ser Gly Gly Ala His Asp Val Ile Ile Cys Asp Glu 20 25 30



| Cys His | Ser | Gla | Asp | <u>ين</u> | Thr | Thr | Ile | Leu | Gly | Ile | Gly | Thr | Val | Leu | |
|---------|-----|-----|-----|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | | 35 | | | | | 40 | | | | | 45 | | | |

Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Xaa 50 55 60

The Pro Pro Gly Ser Val The The Pro His Pro Ash Ile Glu Glu Val

Ala Leu Pro Gin Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala Ile Pro

Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys

Lys Asn Cys Asp Glu Leu 115

- (2) INFORMATION FOR SEQ ID NO: 57:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cONA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE: (B) CLONE: PC-1-48
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 (B) LOCATION: 1..354
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ACCACCGGAG CTTCTATCAC ATACTCCACT TACGGCAAGT TCCTTGCTGA TGGAGGGTGT 60

TCAGGCGGCG CGTATGACGT GATCATATGC GACGAGTGCC ATTCCCAGGA CGCCACCACC 120

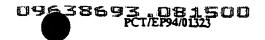
ATTCTTGGGA TAGGCACTGT CCTTGACCAG GCAGAGACGG CTGGAGCTAG GCTĆGTCGTC 180

TTGGNCACGG NCACCCCTCC CGGCAGTGTG ACAACGCCCC ACCCCAACAT CGAGGAAGTG 240

GCCCTGCCTC AGGAGGGGGA GGTTCCCTTC TACGGNAGAG CCATTCCCCT TGCTTTTATA 300

AAGGGTGGTA GGCATCTCAT CTTCTGCCAT TCCAAGAAAA AATGTGATGA ACTT 354

- (2) INFORMATION FOR SEQ ID NO: 58:
 - (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

The The Gly Ala Ser Ile The Tyr Ser The Tyr Gly Lys Phe Leu Ala

1 10 15

Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys Asp Glu

Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr Val Leu 35 40 45

Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Xaa Thr Xaa 50 55 60

The Pro Pro Gly Ser Val The The Pro His Pro Asm Ile Glu Glu Val 65 70 75 80

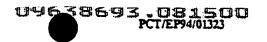
Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Xaa Arg Ala Ile Pro 85 90 95

Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys 100 105 110

Lys Lys Cys Asp Glu Leu Arg Gln Ala Thr Asp Gln Pro Gly Arg Glu 115 120 125

Arg Pro Trp Glu Tyr 130

- (2) INFORMATION FOR SEQ ID NO: 59:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:
 (B) CLONE: PC-1-37
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS



(B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

| ATGGCTTTCA | TGTCTCCGGA | CTTGGAGGTC | ATTACCANCA | CTTGGGTTCT | GGTGGGGGGC | 60 |
|------------|------------|------------|------------|------------|------------|-----|
| GTTGTGGCGA | ccctaicaic | CTACTGCTTG | ACGGTGGGTT | CGGTAGCCAT | AGTESGTAGS | 120 |
| ATCATCCTCT | CTGGGAAACC | TGCCATCATT | NCCGATAGGG | AGGTATTATA | CCAGCAATTT | 190 |
| GATGAGATGG | AGGAGTGCTC | GGCCTCGTTG | CCCTATATGG | ACGAAACACG | TNCCATTGCC | 240 |
| GGACAATTCA | AAGAGAAAGT | GCTCGGCTTC | ATCAGCACGA | CCGGCCAGAA | GGCTGAAACT | 300 |
| CTGAAGCCGG | CAGCCACGTC | TGTGTGGAAC | AAGGCTGATC | AGTTCTGGNC | CACATAC | 357 |

(2) INFORMATION FOR SEC ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: procein
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Met Ala Phe Met Ser Pro Asp Leu Glu Val Ile Thr Xaa Thr Trp Val 1 5 10 15

Leu Val Gly Val Val Ala Thr Leu Xaa Xaa Tyr Cys Leu Thr Val 20 25 30

Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala
35 40 45

Ile Ile Xaa Asp Arg Glu Val Leu Tyr Gln Gln Phe Asp Glu Met Giu 50 55 60

Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Xaa Ile Ala 65 70 75 8J

Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln 85 90 95

Lys Ala Glu Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala 100 105 110

Asp Gln Phe Trp Xaa Thr Tyr Met Trp Asn Phe Ile Ser Gly Ile Gln 115 120 125

- (2) INFORMATION FOR SEQ ID NO: 61:
 - (i) SEQUENCE CHARACTERISTICS:

60

120

130

240

300

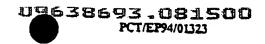
357

| (A) LENGTH: 357 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPCLCGY: linear |
|--|
| (ii) MOLECULE TYPE: CDNA |
| (iii) HYPOTHETICAL: NO |
| (111) ANTI-SENSE: NC |
| (Vii) IMMEDIATE SCURCE: (B) CLONE: PC-1-48 |
| (ix) FEATURE: |
| (A) NAME/KEY: CDS (B) LOCATION: 1357 |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61: |
| ATGGCTTGCA TGTCTGCGGA CCTGGAGGTC ATTACCANCA CTTGGGTTCT GGTGGGGGGC |
| GTTGTGGCGN CCCTGGCGGC CTACTGCTTG ACGGTGGGTT CGGTAGCCAT AGTGGGTAGG |
| ATCATECTET CTGGGAAACT TGCCATCATT CCCGATAGGG AGGCATTATA CCANCAATTT |
| GATGAGATGG AGGAGTGCTC GGCCTCGTTG CCCTATATGG ACGAGACACG TGCCATTGCC |
| GGACAATTCA AAGAGAAAGT GCTCGGCTTC ATCAGCACGA CCGGCCAGAA GGCTGAAACT |
| CTGAAGCCGG CAGCCACGTC TGTGTGGAAC AAGGCTGANC AGTTCTGGGC CACATAC |
| (2) INFORMATION FOR SEQ ID NO: 62: |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 123 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
| (ii) MOLECULE TYPE: protein |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62: |
| Met Ala Cys Met Ser Ala Asp Leu Glu Val Ile Thr Xaa Thr Trp Val |
| Leu Val Gly Gly Val Val Ala Xaa Leu Ala Ala Tyr Cys Leu Thr Val 20 25 30 |
| Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala |

SUBSTITUTE SHEET (RULE 26)

55

Ile Ile Pro Asp Arg Glu Ala Leu Tyr Xaa Gln Phe Asp Glu Met Glu



Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala 65 70 75 80

Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln 85 90 95

Lys Ala Glu Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asm Lys Ala 100 105 110

Xaa Gln Phe Trp Ala Thr Tyr Met Trp Asn Phe Ile Ser Gly Ile Gln
115 120 125

- (2) INFORMATION FOR SEQ ID NO: 63:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr161"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACCGGAGGCC AGGAGAGTGA TCTCCTCC

28

- (2) INFORMATION FOR SEQ ID NO: 64:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: YES
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCP:162"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64: GGGCTGCTCT ATCCTCATCG ACGCCATC (2) INFORMATION FOR SEQ ID NO: 65: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: YES (iii) ANTI-SENSE: NO (ix) FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 1..28 (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPrl63* (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 65: GCCAGAGGCT CGGAAGGCGA TCAGCGCT 28 (2) INFORMATION FOR SEQ ID NO: 66: (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: YES
- (ix) FEATURE:

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- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HC2r164"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GAGCTGCTCT GTCCTCCTCG ACGCCGCA

(2) INFORMATION FOR SEQ ID NO: 67:

28

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genemic)
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_mame= "HCV Primer HCP=23"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CTCATGGGGT ACATTCCGCT

20

- (2) INFORMATION FOR SEQ ID NO: 68:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: YES
 - (ix) FEATURE:

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- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCP=54"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CTATTACCAG TTCATCATCA TATCCCA

27

- (2) INFORMATION FOR SEQ ID NO: 69:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

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|------------|--|
| | 154 |
| (iii | HYPOTHETICAL: YES |
| (iii | ANTI-SENSE: NO |
| (ix) | FEATURE: (A) NAME/KEY: misc_feature (B) LOCATION: 128 (D) OTHER INFORMATION: /standard_name= "HCV Prime HCPrl16" |
| (xi) | SEQUENCE DESCRIPTION: SEQ ID NO: 69: |
| TTTTAAA1 | TAC ATCATGROTG YATG |
| (2) INFO | RMATION FOR SEQ ID NO: 70: |
| (±) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear |
| (ii) | MOLECULE TYPE: DNA (genomic) |
| (iii) | HYPOTHETICAL: YES |
| (iii) | ANTI-SENSE: YES |
| (ix) 1 | FEATIBS. |

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr66"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CTATTATTGT ATCCCRCTGA TGAARTTCCA CAT

33

24

- (2) INFORMATION FOR SEQ ID NO: 71:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: YES
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature



- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPrl18:
- (x1) SEQUENCE DESCRIPTION: SEQ. ID NO: 71:

ACTAGTCGAC TAYTGATCCR CTATRWARTT CCACAT

36

- (2) INFORMATION FOR SEQ ID NO: 72:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (E) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPrl17:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TTTTAAATAC ATCGCRCTGC ATGCA

25

- (2) INFORMATION FOR SEQ ID NO: 73:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: YES
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPrl19:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

ACTAGTOGAC TARTTGCATA GCCKRTTCAT CCAYTG

36

- (2) INFORMATION FOR SEQ ID NO: 74:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPS: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr131:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GGAATTCTAG ACCTCTGGGA YGARAYTGGA ARTG

34

- (2) INFORMATION FOR SEQ ID NO: 75:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr130:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GGAATTCTAG ACGCTAYCAR GCACGTTGYG C

31

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- (2) INFORMATION FOR SEQ ID NO: 76:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid



- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (gen mic)
- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: MC
- (ix) PEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= *HCV Primer HCPr134:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CATATAGATG CCCACTTCCT ATC

2-3

- (2) INFORMATION FOR SEQ ID NO: 77:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: YES
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr3:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GTGTGCCAGG ACCATC

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16 .

- (2) INFORMATION FOR SEQ ID NO: 78:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - '(D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)

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- (iii) HYPOTHETICAL: YES
- (iii) ANTI-SENSE: YES
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /scandard_name= *HCV Primer HC2r4:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GACATGCATG TCATGATGTA

20

- (2) INFORMATION FOR SEQ ID NO: 79:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (3) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr152:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TACGCCTCTT CTATATCGGT TGGGGCCTG

29

- (2) INFORMATION FOR SEQ ID NO: 80:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPrs2:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ATGTTGGGTA AGGTCATCGA TACCCT

26

- (2) INFORMATION FOR SEQ ID NO: 81:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..28
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr41:
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CCCGGGAGGT CTCGTAGACC GTGCA

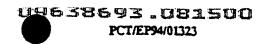
25

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- (2) INFORMATION FOR SEQ ID NO: 82:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: YES
 - (iii) ANTI-SENSE: YES
 - (ix) FEATURE:

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- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard_name= "HCV Primer HCPr40:



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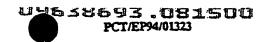
(xi) SEQUENCE DESCRIPTION; SEQ ID NO: 82:

CTATTAAAGA TAGAGAAAGA GCAACCGGG

- (I) INFORMATION FOR SEQ ID NO: 83:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 192 to 203 of the V1 region of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:
 Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu
 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 84:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 85:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single



- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 213 to 223 of the V2 region of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Val Tyr Glu Ala Asp Asp Val Ile Leu His Thr 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 86:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
- (viii) POSITION IN PROTEIN:

 (B) MAP POSITION: positions 213 to 233 of the V2 region of HCV type 5
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Val Tyr Glu Ala Asp Asm Leu Ile Leu His Ala 1 5 10

- (2) INFORMATION FOR SEC ID NO: 87:
 - (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO

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(viii) POSITION IN PROTEIN:
(B) MAP POSITION: positions 230 to 242 of the V3 region of HCV type 3

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Val Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val

- (2) INFORMATION FOR SEQ ID NO: 88:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPCLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 230 to 242 of the V3 region of HCV type 5
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Val Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile

- (2) INFORMATION FOR SEQ ID NO: 89:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 248 to 257 of the V4 region of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Val Arg Tyr Val Gly Ala Thr Thr Ala Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 90:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 248 t 257 of the V4 region of HC/
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ala Pro Ser Leu Gly Ala Val Thr Ala Pro 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 91:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
- - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Arg Pro Arg Arg His Gla Thr Val Gla Thr

- (2) INFORMATION FOR SEQ ID NO: 92:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
- (viii) POSITION IN PROTEIN:

 (B) MAP POSITION: positions 294 to 303 of the V5 region of HCV type 5
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:



Arg Pro Arg Gln His Ala Thr Val Gln Asn 1 5 10

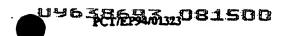
- (2) INFORMATION FOR SEQ ID NO: 93:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGIH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN PROTEIN:
 - (B) MAP POSITION: positions 70 to 78 of RCV type 5
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Gln Pro Thr Gly Arg Ser Trp Gly Gln

- (2) INFORMATION FOR SEQ ID NO: 94:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTY: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: BR33 and BR36
 - (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 230 to 237 of the V3 region of HCV
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Val Gln Asp Gly Asn Thr Ser Thr 1 5

- (2) INFORMATION FOR SEQ ID NO: 95:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single



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- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISCLATE: HD10
- (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 230 to 237 of the V3 region of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

Val Gln Asp Gly Asn Thr Ser Ala

- (2) INFORMATION FOR SEQ ID NO: 96:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: BR36
 - (viii) POSITION IN PROTEIN:
- (B) MAP POSITION: positions 248 to 257 of the V4 region of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser

- (2) INFORMATION FOR SEQ ID NO: 97:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: BR36

```
(viii) POSITION IN GENOME:
(B) MAP POSITION: Positions 1688 to 1707 of HCV type 3
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys Glu Val Leu Tyr Gin
15

Gln Tyr Asp Glu 20

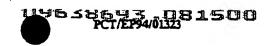
- (2) INFORMATION FOR SEQ ID NO: 98:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HD10
 - (viii) POSITION IN GENOME:
 - (B) MAP POSITION: positions 1688 to 1707 of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

Leu Gly Gly Lys Pro Ala Leu Val Pro Asp Lys Glu Val Leu Tyr Gln
1 10 15

Gin Tyr Asp Glu 20

- (2) INFORMATION FOR SEQ ID NO: 99:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN GENOME:
 - (B) MAP POSITION: positions 1712 to 1731
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

.



Ser Gln Ala Ala Pro Tyr Il Glu Gln Ala Gln Val Ile Ala His Gln l 5 10 15

Phe Lys Glu Lys

- (2) INFORMATION FOR SEQ ID NO: 100:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LZNGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: BR36
 - (viii) POSITION IN GENOME:
 - (B) MAP POSITION: positions 1724 to 1743 of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Ile Ala His Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala

1 5 10 15

Thr Gln Gln Gln 20

- (2) INFORMATION FOR SEQ ID NO: 101:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (C) INDIVIDUAL ISOLATE: HD10
 - (viii) POSITION IN GENOME:
 - (B) MAP POSITION: positions 1724 to 1743 of HCV type 3
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

Ile Ala His Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala

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Thr Gln Gln Gln

- (2) INFORMATION FOR SEQ ID NO: 102:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANGEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: pepcide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN GENOME:
 - (B) MAP POSITION: positions 1688 to 1707 of HCV type 5
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Ala Leu Tyr Gln
1 10 15

Gla Phe Asp Glu 20

- (2) INFORMATION FOR SEQ ID NO: 103:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN GENOME:
 - (B) MAP POSITION: positions 1688 to 1707
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Gln
1 5 10 15

Gln Phe Asp Glu

- (2) INFORMATION FOR SEQ ID NO: 104:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (viii) POSITION IN GENOME:
 - (B) MAP POSITION: position 1712 to 1731 of HCV type 5
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln
1 5 10 15

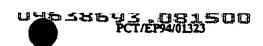
Phe Lys Glu Lys

- (2) INFORMATION FOR SEQ ID NO: 105:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (viii) POSITION IN GENOME:
 - (B) MAP POSITION: positions 1724 to 1743 of HCV type 5
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

Ile Ala Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr 1 5 10 15

Gly Gln Lys Ala 20

- (2) INFORMATION FOR SEQ ID NO: 106:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO



| 1 | i | i | í | ١ | A | N | rt | _ | c | = | te | = | | | 10 |
|---|---|---|---|---|---|----|----|---|---|---|----|---|---|---|----|
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| (vii) | IMMEDIATE SOURCE: | |
|-------|-------------------|--|
| | (B) CTONE, CD40 3 | |

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

| C T S | er T | CT G hr V | TA A | CC G | lu L | AG G ys A | AC A sp I | TC A | GG G | TC G | AG G lu G | kG G Lu G | AG G | TC T | AT Y= | 46 |
|----------------|-------|--------------|------|------------|------|--------------|--------------|------|------|------|--------------|--------------|------|------|----------|-------|
| | 1 | | | | 5 | | | | | 10 | | | | : | 15 | |
| CAG | TGT | TGT | GAC | CTG | GAG | ccc | GAA | GCC | CGC | מגג | GC2 | ښند ۲ | 300 | ccc | ~~ | 0.4 |
| Gln | Сув | Cys | Asp | Leu | Glu | Pro | Glu | Ala | Ars | Lvs | 2:4 | 710 | Thr | 272 | Cin | 94 |
| | | | - | 20 | • | | | | 25 | | | | | 30 | De 2 | • |
| ACA | GAG | AGA | CTC | TAC | GTG | GGC | GGT | ccc | ATG | CAT | عند | AGC | AAG | 455 | G2C | 142 |
| The | Glu | Arg | Leu | Tyr | Val | Gly | Gly | Pro | Met | His | As: | Ser | Lvs | Glv | Ase | *** |
| | | | · 35 | | | • | • | 40 | | | | | 45 | | | |
| CTG | TGC | GGG | TAT | CGC | AGA | TGT | CGC | GCA | AGC | GGC | برت | 720 | ACC. | 3.00 | 200 | 190 |
| Leu | Cys | Gly | Tyr | Arg | Arg | Cys | Arg | Ala | Ser | Gly | Va: | TV | Thr | The | Se- | , 190 |
| | | 50 | _ | _ | _ | - | 55 | | | • | | 60 | | | | |
| ميت | | | | | | | | | | | | | | | | |
| Dha | Gly | AAC | ACA | CTG | ACG | TGC | TAC | CIC | AAA | GCC | TCA | GCC | GCT | ATC | AAA | 238 |
| | 55 | ASU. | 1412 | Leu | 110 | 70 | ryr | ren | Lys | λia | Ser 75 | λia | Ala | Ile | Lys | |
| | • | | | | | ,, | | | | | /2 | | | | | |
| GCG | GCG | GGG | CTG | AGA | GAC | TGC | ACC | ATG | TTG | GTC | TGT | GGT | GAT | GAC | CTG | 286 |
| Ala | Ala | Gly | Leu | Arg | çzƙ | Суз | Thr | Met | Leu | Val | Cys | Gly | Asp | Aso | Leu | 200 |
| 80 | | | | | 85 | | | ٠ | | 90 | • | - | • | • | 95 | |
| ستن | | | | | | | | | | | | | | | | |
| Va: | G I C | TIO | GCT | GAG | AGC | GAT | GGC | GTA | GAG | GAG | GAC | ککک | CGA | CCC | CTC | 334 |
| 407 | V4.2 | 176 | wta | Glu 100 | ser | ASP | GIA | Vai | | GTA | ASD | Lys | Arg | | Leu | |
| | | | | 100 | | | | | 105 | | | | | 110 | | |
| GGA | GCC | | | | | | | | | | | | | | | 340 |
| Gly | Ala | | | | | | | | | | | | | | | 540 |

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln 1 5 15

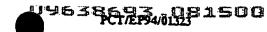


Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala L u Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu 40 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Lys Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val 85 Val Ile Ala Glu Ser Asp Gly Val Glu Giu Asp Lys Arg Pro Leu Gly 100 105 Ala (2) INFORMATION FOR SEQ ID NO: 108: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 340 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iii) ANTI-SENSE: NO (vii) IMMEDIATE SOURCE: (B) CLONE: G3116-3-5 (ix) FEATURE: (A) NAME/KEY: CDS

(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTA TAT Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr 5 10 CAG TGT TGT GAC CTG GAG CCC GAG GCC CGC AGA GCA ATT ACC GCC CTA Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Thr Ala Leu 20 ACA GAG AGA CTC TAC GTG GGC GGT CCC ATG CAT AAC AGC AGG GGA GAC Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp 35 40



| CIG | TGC | GGG | TAT | CGC | AGA | TGC | CGT | GCG | AGC | GGC | GTC | TAC | ACC | ACC | AGC | 190 |
|------------------|------------------|------------|------------|-------------------|------------------|------------------|------------|------------|-------------------|--------------------|------------------|------------|------------|-------------------|------------------|-----|
| Leu | Cha | Gly 50 | Tyr | Arg | Arg | Cys | Arg 55 | Ala | Ser | Gly | Val | 90 LAZ | Thr | Thr | Ser | 434 |
| TTC Phe | GGG Gly 65 | AAC Asn | ACA Thr | CTG Leu | ACG Thr | TGC Cys 70 | TAT Tyt | CTC Leu | aaa Lys | GCC Ala | TCA Ser 75 | GCC Ala | GCT Ala | ATC Ile | aga Arg | 238 |
| GCG Ala 80 | GCG Ala | GG3 Gly | CTG Leu | YLA YLA | GAC Asp 85 | TGC Cys | ACC Thr | ATG Met | TTG Leu | GTC Val 90 | TGT Cys | GGT Gly | GAT Asp | gac Asp | CTG Leu 95 | 286 |
| GTC Val | GTC Val | ATT Ile | GCT Ala | GAA Glu 100 | AGC Ser | GAT QeA | GGC Gly | GTA Val | GAG Glu 105 | GJ <i>n</i> GYG | GAC Asp | AAA Lys | CGY | GCC Ala 110 | CTC Leu | 334 |
| GGA Gly | | | | | | | | | | | | | | | | 340 |

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Thr Ala Leu Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala 65 70 75 80

Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 110:

| | | (| A) L | ENGI | H: 3 | 40 b | ase | pair | ·S | | | | | | | |
|--------------|------------|------|--|--------------|-------|-------------|-------|-------|-----------|------------|------|-------|-------------|------------|------|-----|
| | | (| B) I | YPE: | unc | leic | aci | d | | | | | | | | |
| | | (| C) S | TRAN | DEDN | ESS: | sin | gle | | | | | | | | |
| | | | | OPOL | | | | • | | | | | | | | |
| | (ii |) мо | LECU | LE T | YPE: | CDN | Ά | | | | | | | | | |
| | (iii |) HY | Poth | ETIC | AL: | NO | | | | | | | | | | |
| | (iii |) An | TI-S | ense | : NO | | | | | | | | | | | |
| | (vii | | | ate Lone | | | 3-8 | | | | | | | | | |
| | (ix | | ATUR | | | | | | | | | | | | | |
| | | | | ame/ Ocat | | | | | | | | | | • | | • |
| | | , | J | · · · · | -04. | • | 340 | | | | | | | | | |
| | lasi i | | OFFICE AND ADDRESS OF THE ADDRESS OF | CC D | | | ~~~ | | | | | | | | | |
| | 1. | , 3E | 2023 | CE D | esca. | 1 e 1 1 1 | ON: : | SEQ . | א סנ | 0: 1: | 10: | | | | | |
| C T | CC A | CI G | TA A | CC G | AA AA | AA G | ac a | TC A | GG G | TC G | AG G | AG G | AG G | TA T | AT . | 46 |
| S | er Ti | ır V | al T | hr G | | ys A | sp I | le A | rg V | al G | lu G | lu G | lu V | al T | Az , | |
| | 1 | | | | 5 | | | | | 10 | | | | ; | 15 | |
| CAG | TGT | TGT | GAC | CTG | GAG | CCC | GZZ | 600 | .ccc | 330 | C#1 | > THE | 200 | | ~ | |
| Gln | Cys | Cvs | Asp | Leu | Glu | Pro | Gl: | Ala | 250 | Live | Val | TIA | The | 313 | CIA | 94 |
| | • | - 2 | • | 20 | | | | | 25 | 273 | 447 | -75 | 1114 | 30 | ### | |
| | | | | | | | | | | | | | | | | |
| ACA | GAG | AGA | CIC | TAT | GTG | GGC | GGT | CCC | ATG | CXT | AAT | AGC | AAA | GGA | GAC | 142 |
| Inr | GIU | Arg | Leu 35 | Tyr | Val | Gly | Gly | | Met | His | λsn | Ser | | Gly | Asp | |
| | | | 33 | | | | | 40 | | | | | 45 | | | |
| CTG | TGC | GGG | TAT | CGC | AGA | TGC | CGC | GCA | AGC | GGC | GTC | TAC | ACC | ACC | AGC | 190 |
| Leu | Cys | Gly | Tyr | Arg | Arg | Cys | Arg | Ala | Ser | Gly | Val | Tyr | Thr | The | Ser | |
| | | 50 | | | | | 55 | | | | | 60 | | | | |
| 7-T C | aga | 220 | 3/23 | CTC | B.CC | TCC | ~ ~ | CTC. | | 600 | 841 | | | | AGG | |
| Phe | Glv | Asn | スピス | Leu | Th- | CA4 | TV | T.O. | Lva | GCC 31- | TCA | GCC | GCC | ATC | AGG | 238 |
| | 65 | | | | | 70 | -7- | | <i></i> , | ~~ | 75 | VT. | ALG | 775 | λig | |
| ece | TCA | ccc | CTC: | AGA | 636 | T CC | 3 CT | n ~~ | ~~~ | cmc | | | | | | |
| Ala | Ser | Glv | Leu | Arg | Aco | CAR | Th- | Mar | LLG | UIL | TAI | GGT | GAC | GAC | CTG | 296 |
| 80 | | , | | , | 85 | -,- | | | | 90 | . y- | GLY | vañ | rap | 95 | |
| ^ | | | | | | | | | | | | | | | | |
| GTC Val | GTC Val | ATT | GCC | GAG | AGC | GAT | GGC | GTA | GAG | GAG | GAC | AAA | CGA | GCC | CTC | 334 |
| 167 | 497 | 774 | wra | Glu 100 | se: | ASD | Giğ | vai | 105 | GIU | ÇZA | Lys | Arg | Ala 110 | ren | |
| | | | | | | | | | -43 | | | | | 110 | | |
| | GTC | | | | | | | | | | | | | | | 340 |
| C1 1/ | Wal | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

Ser Thr. Val Thr Giu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
1 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala 65 70 75 80

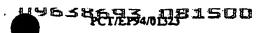
Ser Gly Leu Arg Asp Cys Thr Met Leu Val Tyr Gly Asp Asp Leu Val

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
100 105 110

Val

- (2) INFORMATION FOR SEQ ID NO: 112:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (111) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE:
 - (B) CLONE: GB358-3-3
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..340
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:
- C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTG TAT

46



| Ser Thr Val Th | r Glu Lys Asp I | ie Arg Val Glu Glu | Glu Vai Tyr |
|-----------------|-----------------------|---------------------------|----------------------|
| 1 | 5 | 10 | 15 |
| | | GCC CGC AAG GCA AT | |
| Gln Cys Cys Asp | Leu Glu Pro Glu 20 | Ala Arg Lys Ala Il 25 | |
| | 20 | . 23 | 30 |
| | | CCC ATG CAT AAC AG | |
| Thr Glu Arg Leu | Tyr Val Gly Gly | Pro Met His Asn Se | r Lys Gly Asp 45 |
| | | 40 | |
| | | GCA AGC GGC GTC TA | |
| Leu Cys Gly Tyr | Arg Arg Cys Arg | Ala Ser Gly Val Ty | |
| | | · | • |
| | | CTC AAA GCC TCA GC | |
| Phe Gly Asn Thr | Leu Thr Cys Tyr | Leu Lys Ala Ser Al | a Ala Ile Arg |
| 33 | ., | ,, | • |
| | | ATG TTG GTC TGT GG | |
| Ala Ala Gly Leu | Ary Asp Cys Thr | Met Leu Val Cys Gl | y Asp Asp Leu 95 |
| | . 63 | 30 | 33 |
| | | GTT GAG GAG GAC AA | |
| | Glu Ser Asp Gly | Val Glu Glu Asp Ly 105 | s Arg Ala Leu 110 |
| | *** | *** | *** |
| GGA GCC | | | 340 |
| Gly Ala | | | |

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Glm 1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe 50 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala 65 70 75 80



286

Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly

Ala

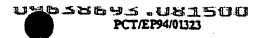
(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: GB549-3-6
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

| C TCC | ACG | GTG | ACC | GAA | AGG | GAT | ATC | AGG | ACC | GAG | GλA | GAG | ATC | TAC | 46 |
|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Ser | Inr | val | THE | GIA | Arg | qzA | Ile | Arg | The | Glu | Glu | Glu | Ile | Tyr | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

- CAG TGC TGC GAC CTG GAG CCC GAA GCC CGC AAG GTG ATA TCC GCC CTA
 Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu
 20 25 30
- ACG GAA AGA CTC TAC GTG GGC GGT CCC ATG TAC AAC TCC AAG GGG GAC
 Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp
 35
 40
 45
- CTA TGC GGG CAA CGG AGG TGC CGC GCA AGC GGG GTC TAC ACC ACC AGC
 Leu Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser
 50 55
- TTC GGG AAC ACT GTA ACG TGT TAT CTC AAG GCC GTT GCG GCT ACT AGG
 Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg
 65
- GCC GCA GGT CTG AAA GGT TGC AGC ATG CTG GTT TGT GGA GAC GAC TTA
 Ala Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu
 80 90 95



GTC GTC ATC TGC GAG AGC GGC GGC GTA GAG GAG GAT GCA AGA GCC CTC

Val Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu

100 105 110

CGA GCC Arg Ala

340

- (2) INFORMATION FOR SEQ ID NO: 115:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gln
1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg Ala 65 70 75 80

Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg
100 105 110

Ala

- (2) INFORMATION FOR SEQ ID NO: 116:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

| (vii) | IMMEDIAT | E SOURCE: |
|-------|----------|---------------|
| | (B) CLOI | TE: GR809-3-1 |

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..340

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

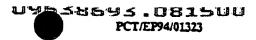
| C | rcc ; Ser 1 | hr (| FTG A /al T | hr G | AG A lu A S | LTG A | iac a | TC A | iys V | TC G al G | iaa o | iaa G | AA G Hu V | TC 1 al 1 | AT Yr 15 | 46 |
|------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------|-------------------|------------------|------------------|------------------|--------------------|-------------------|------------------|-----|
| CAC Glr | TGT Cys | TGT Cys | GAT Asp | CTG Leu 20 | GAG Glu | Pro CCC | GAG Glu | GCC Ala | CGC Arg | Lys | GTA Val | ATA Ile | GCC Ala | GCC Ala | CTC Leu | 94 |
| | - | · ALG | CTC Leu 35 | TYT | AST | Giy | GIÅ | PTO | Met | His | nek | Ser | Lys 45 | Gly | ģek | 142 |
| CTT | TGC | GGG Gly 50 | TAT | CGT Arg | AGA AIG | TGC Cys | CGC Arg 55 | GCG Ala | AGC Ser | GGC | GTA Val | TAC Tyr 60 | ACC Thr | ACC Thr | AGC Ser | 190 |
| TTC Phe | GGG Gly 65 | AAC Asn | ACA Thr | ATG Met | ACG Thr | TGC Cys 70 | TAC Tyr | CTT Leu | AAG Lys | GCC Ala | TCA Ser 75 | GCA Ala | GCC Ala | ATC Ile | AGG Azg | 238 |
| GCT Ala 80 | GCG Ala | GGG Gly | CTA Leu | AAG Lys | GAT Asp 85 | TGC Cys | ACC Thr | ATG Met | CTG Leu | GTT Val 90 | TGC Cys | GGT Gly | GAC A sp | GAC Asp | CTA Leu 95 | 286 |
| GTC Val | GTG Val | ATC Ile | GCC Ala | GAG Glu 100 | AGC Ser | GGT Gly | GGC | GTT Val | GAG Glu 105 | GAG Glu | GAC Asp | aaa Lys | CGA Arg | GCC Ala 110 | CTC Leu | 334 |
| GGA Glv | | | | | • | | | | | | | | | | | 340 |

(2) INFORMATION FOR SEQ ID NO: 117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu Glu Val Tyr Gln

1 5 10 15



| Cys | Cys | Asp | Leu | Glu | Pro | Glu | Ala | Arg | Lys | Val | Ile | Ala | Ala | Leu | The |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | | | 20 | | | | | 25 | - | | | | 30 | | |

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe 50 60

Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala 65 70 75 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val

Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: GB358-4-1
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 5 10 15

CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG 96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val

GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

35

40

45



| TCT | ATC Ile 50 | TTC Phe | CTC | TTG Leu | GCA Ala | CTT Leu SS | CTT | TCG Ser | TGC Cys | CTG Leu | ACT Thr 60 | GTT Val | CCC | ACC Thr | TCG Ser | | 192 |
|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|---|-----|
| GCC Ala 65 | Val | AAC Asn | TAT Tyr | CGC | AAT ASD 70 | GCC Ala | TCG Ser | GGC Gly | ATC Ile | TAT Tyr 75 | CAC His | ATC Ile | ACC Thr | AAT Asn | GAC Asp 80 | | 240 |
| TGC Cys | CCG Pro. | AAC Asa | TCG Ser | AGC Ser 85 | ATA Ile | GTG Val | TAC Tyr | GAG Glu | ACC Thr 90 | GAG Glu | CAC His | CAC His | ATC Ile | CTA Leu 95 | CAC His | | 288 |
| CTC | CCA Pro | GGG Gly | TGT Cys 100 | TTA Leu | PT0 | CA2 ICC | GTG Val | AGG Arg 105 | GIT Val | GGG Gly | aat Asd | CAG Gl:1 | TCA Ser 110 | CGC | TGC Cys | | 336 |
| TGG Trp | GTG Val | GCC Ala 115 | CTC Leu | ACT Thr | CCC | ACC Thr | GTG Val 120 | GCG Ala | GCG Ala | CCT Pro | TAC Ty= | ATC Ile 125 | GGC Gly | GCT Ala | CCG Pro | • | 384 |
| CII | GAA Glu 130 | TCC Ser | CTC Leu | CGG Arg | AGT Ser | CAT His 135 | GTG Val | GAT QaA | CTG Leu | ATG Met | GTA Val 140 | GGT Gly | GCC Ala | GCT Ala | ACT Thr | | 432 |
| GCG Ala 145 | TGC Cys | TCC Ser | GCT Ala | CTT Leu | TAC- Ty - 150 | ATC Ile | GGA Gly | GAC Asp | CTG Leu | TGC Cys 135 | GGT Gly | GGC Gly | GTA Val | TTC Phe | TTG Leu 160 | | 480 |
| GTT Val | GGT Gly | CAG Gln | ATG Met | TTC Phe 165 | TCT Ser | TTC Phe | CAG Gln | CCG Pro | CGG Arg 170 | CGC | CAC His | TGG Txp | ACT Thr | ACG Thr 175 | CAG Gln | | 528 |
| | | | TGT Cys 180 | | | | | | | | | | | | A | | 574 |

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser

50

55

60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His Hi Ile Leu His 85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys

Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro 115 120 125

Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140

Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 155 160

Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg 180 185 190

- (2) INFORMATION FOR SEQ ID NO: 120:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vii) IMMEDIATE SOURCE: (B) CLONE: GB549-4-3
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..574
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

ACG TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 10 15

CCT GTG GGT GGC GTC GCC AGG GCC TTG GCA CAT GGT GTC AGG GCC GTG

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val

20

25

30

| GIU | Asp | 35 | | Asn | Tyr | Ala | Thr 40 | Gly | Asn | Leu | Pro | Gly 45 | Cys | Ser | Phe | | 144 |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|---|-----|
| Ser | Ile 50 | Phe | Leu | Leu | Ala | Leu 55 | Leu | Ser | CÀ2 | Leu | Thr 60 | Val | Pro | Ala | Ser | | 192 |
| 65 Ala | Gln | His | TAC | Arg | Asn 70 | Ile | Ser | Gly | Ile | 75 | His | Val | Thr | Asn | Asp 80 | | 240 |
| TGC Cys | CCC Pro | AAC Asn | TCT | AGT Ser 85 | ATA Ile | GTG Val | TAT Tyr | GAA Glu | GCT Ala 90 | GAC Asp | CAT His | CAT His | ATC Ile | ATG Met 95 | CAT His | | 288 |
| CTA Leu | δ≟ο CCY | GGG Gly | TGT Cys 100 | GTG Val | CCT Pro | TGC Cys | GTG Val | AGA Arg 105 | ACC Thr | GGG Gly | AAC Asn | ACC Thr | TCG Ser 110 | CGC Arg | TGC Cys | • | 336 |
| TGG | GTT Val | CCT Pro 115 | TTA Leu | ACA Thr | Pro | ACT Thr | GTG Val 120 | GCT Ala | GCC Ala | Pro CCC | TAT Tyt | GTT Val 125 | GGC Gly | GCG Ala | CCG Pro | | 384 |
| CTC | GAA Glu 130 | TCC Ser | ATG Met | Arg | CGG Arg | CAC His 135 | GTG Val | GAC Asp | TIX Leu | ATG Met | GTG Val 140 | GGT Gly | GCC Ala | GCC Ala | ACC Thr | • | 432 |
| GTC Val 145 | TGC Cys | TCG Ser | GCC Ala | CTG Leu | TAC Tyr 150 | ATC Ile | GGA Gly | GAC Qak | CTT | TGC Cys 155 | GGA Gly | GGT Gly | GTC Val | TTC Phe | CTG Leu 160 | | 480 |
| GTC Val | GGG Gly | CAG Gln | ATG Met | TTC Phe 165 | ACC Thr | TTC Phe | CGG Arg | CCG Pro | CGC Arg 170 | CGC Arg | CAT His | Icc Icc | ACT Thr | ACC Thr 175 | CAG Gln | | 529 |
| GAC Asp | TGC Cys | AAC Asn | TGC Cys 180 | TCT Ser | ATC Ile | TAT Tyr | GAT Asp | GGC Gly 185 | CAC His | ATC Ile | ACC Thr | GGC Gly | CAT His 190 | AGA Arg | A | | 574 |

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val



Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

183

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys

Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro 115 120 125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 155 160

Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg 180 185 190

(2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 574 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE: (B) CLONE: GB809-4-3
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..574
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC

49

184

| | | | | | • | | | | 10 | , | | | | 19 | | |
|------------------|--------------|------------|-------------------|----------------------|----------------------|----------------|------------|-----------------------|------------------|------------------|------------|------------------|------------|------------------|------------------|-------|
| | | | | 20 | | a AL | i wra | Let 15 | i Ala | l His | Gly | / Val | Arg | , Ala | GTG Val | 96 |
| GA(G1: | g Ga 1 As | | G λ? y II 5 | T AR le As | e ty: | T GC: T Ale | AC Thi | GTA | AAT Asn | CTI Leu | CCC Pro | GGT Gly 45 | CAS | TCI Se: | TTC Phe | 144 |
| Ser | AT: F Ile | | C CI | C CI | G GC: u Ala | Leu 55 | reu | TCG Ser | TGC | CTC | ACT Thr | Va1 | Pro | GCG Ala | TCA Ser | 192 |
| GCI Ala 63 | GAC | CA Hi | C TA S Ty | r Ar | S AAT S AST 70 | . MIG | TCG Ser | GGC | ATC Ile | TAT Ty= 75 | CAC His | ATC Ile | ACC Thr | TAA neA | GAC Asp 80 | . 240 |
| TGT Cys | Bro CCC | AA: | T TC | C AG: r Se: 8: | GTA Val | GTC Val | TAT | GAA Glu | ACT Thr 90 | GAC Asp | CAC His | CAT His | ATA Ile | TTG Leu 95 | CAC His | 288 |
| | | , | 10 |) | CCC. Pro | Cys | Vai | Arg | Aia | Giy | Asn | Val | Ser | yrâ | Cys | , 336 |
| 44, | •••• | 115 | va. | نه د | CCT Pro | ruz | 120 | Ala | Ala | Val | Ser | Mec 125 | ğsp | Ala | Pro | 384 |
| | 130 | - | 2.10 | ~ _9 | CGG Arg | 135 | YEY | ASp | Leu | Me: | Val 140 | Glγ | Ala | λla | Thr | 432 |
| 145 | - 73 | 36. | 441 | . Dea | TAT Ty= 150 | vai | GIÀ | Asp | Leu | Cys 155 | Gly | Gly | Ala | Phe | Leu 160 | 480 |
| | u., | 9111 | Mec | 165 | ACC | Pne | GIN | Pro | Arg 170 | Arg | His | Trp | Thr | Thr 175 | Gln | 529 |
| GAT Asp | TGT Cys | AAT Asn | TGC Cys 180 | TCC | ATC Ile | TAT Tyr | Thr | GGC Gly 185 | CAT . His : | ATC Ile | ACC Thr | Gly : | CAC His | AGG Arg | A | 574 |

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:



Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pr Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Ph 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys
100 105 110

Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro 115 120 125

Leu Glu Ser Phe Arg Arg His Val Asp Leu Mec Val Gly Ala Ala Thr 130 135 140

Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu 145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg 180 185 190

- (2) INFORMATION FOR SEQ ID NO: 124:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..31
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HCP:206"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TGGGGATCCC GTATGATACC CGCTGCTTTG A

- (2) INFORMATION FOR SEQ ID NO: 125:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: YES
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..30
 - (D) OTHER INFORMATION: /standard_name= "HCV Primer HcPr207"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GGCGGAATTC CTGGTCATAG CCTCCGTGAA

30

31

- (2) INFORMATION FOR SEQ ID NO: 126:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB358
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile

1 10

- (2) INFORMATION FOR SEQ ID NO: 127:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide

- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Amino acid
 - (C) INDIVIDUAL ISOLATE: GB549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Glin His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val

- (2) INFORMATION FOR SEQ ID NO: 128:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amizo acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPCLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Amino acid
 - (C) INDIVIDUAL ISOLATE: GB809
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile 1 5 10

- (2) INFORMATION FOR SEC ID NO: 129:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISCLATE: GB358
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Val Tyr Glu Thr Glu His His Ile Leu His Leu 1 5 10

(2) INFORMATION FOR SEQ ID NO: 130:

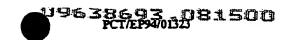
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: pepcide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) CRGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Val Tyr Glu Ala Asp His His Ile Met His Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 131:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISCLATE: GB809
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Val Tyr Glu Thr Asp His His Ile Leu His Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 132:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB358



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Val Arg Val Gly Asn Gln Ser Arg Cys Trp Val Ala Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 133:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB549
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Val Arg Thr Gly Asn Thr Ser Arg Cys Trp Val Pro Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 134:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB809
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Val Arg Ala Gly Asn Val Ser Arg Cys Trp Thr Pro Val 1

- (2) INFORMATION FOR SEQ ID NO: 135:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino ficids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB358
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:
- Ala Pro Tyr Ile Gly Ala Pro Leu Glu Ser
 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 136:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB549
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:
 - Ala Pro Tyr Val Gly Ala Pro Leu Glu Ser 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 137:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB809
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:
 - Ala Val Ser Met Asp Ala Pro Leu Glu Ser 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MCLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISCLATE: GB358 and GB809
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

Gln Pro Arg Arg His Trp Thr Thr Gln Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 139:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: amino acid
 - (C) INDIVIDUAL ISOLATE: GB549
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Arg Pro Arg Arg His Trp Thr Thr Gln Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 140:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB549
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Arg Pro Arg Arg His Trp Thr Thr Gln Asp 1 5

- (2) INFORMATION FOR SEQ ID NO: 141:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGGGATATGA TGATGAACTG GTC

23

- (2) INFORMATION FOR SEQ ID NO: 142:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: YES
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CCAGGTACAA CCGAACCAAT TGCC

34

- (2) INFORMATION FOR SEQ ID NO: 143:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 957 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

| (ii) MOLECULE T | YPE: | ANCO |
|-----------------|------|------|
|-----------------|------|------|

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..957

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

| | •••• | | | | | | | | | | | | | | | |
|------------------|------------------|------------------|------------------|-----------------|--------------------|-----------------------|-------------------|------------------|------------------|---------------------|-------------------|------------------|------------------|------------------|-------------------------|-----------|
| ATG Met 1 | AGC Ser | ACA Thr | TAA Dea | CCI Pro 5 | lys Lys | bro CCI | CAA Gla | AGA Arg | AAA Lys 10 | ACC Thr | AAA Lys | AGA Arg | AAC Asn | ACT Thr 15 | AAC Asn | 43 |
| CGC Arg | CGC Arg | CCY 510 | CAG Gln 20 | GAC Asp | GTC Val | AAG Lys | TTC Phe | CCG Pro 25 | GGC Gly | G1À GGI | GGC Gly | CAG Gln | ATC Ile 30 | GTT Val | Gly | 96 |
| GGA Gly | GTA Val | TAC Tyr 35 | Leu | TTG Leu | 510 CCC | Arg CGC | AGG Arg 40 | GGC Gly | B10 CCC | YLâ CGG | TTG Leu | GGT Gly 45 | GTG Val | Arg | GCG Ala | 144 |
| ACG Thr | AGG Arg 50 | Lys | ACT | TCC Ser | GAG Glu | CGG Arg 55 | TCC Ser | CAG Gln | CCA Pro | Arg | GGG Gly 60 | AGG Afg | CGC Arg | CAG Gln | 513 CCC | 192 |
| ATC Ile 65 | Pro | AAA Lys | GAT Asp | CGG | CGC Arg 70 | CCC | ACT Thr | GGC | rys | TCC Ser 75 | TGG Trp | GGA | Lys Lys | CCA Pro | GGA Gly 80 | 240 |
| TAC | CCT | Tro | CCC Pro | CTG Lev | Tyr | GJÀ GGG | AAT Asd | GAG Glu | GGC Gly | Leu | GGC | TGG Trp | GCA Ala | GGG Gly 99 | TGG TIP | 288 |
| CTC | CTG Lev | TCC Ser | Pro 100 | Arg | GGG Gly | TCT Set | CGC | Pro 105 | se: | TGG Trp | GGC Gly | CCF | ACT Thr | . AS | 510 5 CCC | 336 |
| CGG Arg | CAC His | AGG Arg | 3 Se | CGG | C AAC g Ast | TTC | GG1 Gly 120 | Ly | GTC S Val | C ATO | GA1 | T ACC | r Let | r ac | G TGT E Cys | 384 |
| GG(| TT: / Pho | e Al | C GA | C CT | C ATG | G GGG E Gly 13: | i iv | C ATO | e Pro | T GTO | GT(1 Va 14 | I GI | c GC | a Pr | A GTT o Val | 432 |
| GG' G1: | y Gl | T GT y Va | C GC 1 Al | c AG a Ar | A GC g Al 15 | a Le | C GC | G CA a Hi | T GG s Gl | C GTO y Va 15 | l Ar | λ GT g Va | T CT | G GA | 249 A. ÇeA v. 160 | |

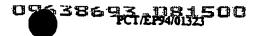
| GG G1 | G AT. y Il | AA A Baa | C TA | F GC2 F Ala 165 | 1444 | GGG Gly | AAC AST | TTO Lev | 9 CCC | GL | TG(Cys | TCC Ser | TT: | TCT Ser 175 | Ile | | 528 |
|-------------------|-------------------|-------------------|-------------------|-----------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|---|-----|
| Pho | TT) | I TO | G GCC | CTG Leu | CTA Leu | Ser | Cys | Ile 185 | Th | Val | . Pro | GTC Val | TCC Ser 190 | Gly | TTG Leu | | 576 |
| CA(| GTC Val | Ly: | , mar. | ACC Thr | AGC Ser | AGC Ser | TCT Ser 200 | TYT | ATG Met | GTA Val | ACC | AAT Asn 205 | GAC Asp | TGC Cys | CAG Gln | | 624 |
| AAC | AGT Ser 210 | | : ATC | GTC Val | 1cc 1cc | CAG Gln 215 | CTC | AGG | GAT Asp | GCT | GTT Val 220 | Leu | CAC His | GTC Val | CCC Pro | | 672 |
| GGG Gly 225 | -,- | GTC Val | CCT Pro | TGT Cys | GAG Glu 230 | GAG Glu | AAG Lys | ej À eec | AAC Asn | ATA Ile 235 | TCC Ser | CGC Arg | TGT Cys | Teg Trp | ATA Ile 240 | - | 720 |
| CCG Pro | GTT Val | TCG | Pro | AAT Asn 245 | λτλ Ile | GCT Ala | GTG Val | AGC Ser | CAA Gln 250 | CCT Pro | GGT Gly | GCG Ala | CTT Leu | ACC Thr 255 | A AG Lys | | 763 |
| GCC | CTG Leu | CGG Arg | ACG Thr 260 | CAT | ATT Ile | GAT Asp | ACC Thr | ATC Ile 265 | ATT Ile | GCA Ala | TCC Ser | GCT Ala | ACG Thr 270 | TIT Phe | TGC Cys | | 816 |
| TCT Ser | GCC Ala | CTG Leu 275 | TAC Tyr | ATA Ile | GJ Y | Asp | CTG Leu 280 | TGT Cys | GGC Gly | GCG Ala | GTG Val | ATG Met 285 | TTG Leu | GCT Ala | TCT Ser | | 864 |
| ~ | GTC Val 290 | TTC Phe | ATC Ile | ATC Ile | ser | CCC Pro 295 | CAG Gln | CAT His | CAT His | AAG Lys | TTT Phe 300 | GTC Val | CAG Gln | GAC Asp | TGC Cys | | 912 |
| AAC Asn 305 | TGT Cys | TCC Ser | ATA Ile | TAC Tyr | Pro (| GGC (Gly) | CAC . Eis | ATC Ile | Thr | GGA Gly 315 | CAT His | CGG Arg | ATG Mec | GCG Ala | | | 957 |

(2) INFORMATION FOR SEQ ID NO: 144:

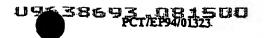
- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 319 amino acids
 - (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15

Arg Arg Pro Gln Asp Val Lys ?he Pro Gly Gly Gly Gln Ile Val Gly 20 25 30



- Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala 35 40 45
- Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
 50 55 60
- Ile Pro Lys Asp Arg Arg Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly 65 70 75 80
- Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp 85 90 95
- Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
- Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
 115 120 125
- Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val
- Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp 145 150 155 160
- Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile 165 170 175
- Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Gly Leu 180 185 190
- Gin Val Lys Asn Thr Ser Ser Ser Tyr Met Val Thr Asn Asp Cys Gin 195 200 205
- Asn Ser Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro 210 215 220
- Gly Cys Val Pro Cys Glu Glu Lys Gly Asn Ile Ser Arg Cys Trp Ile
 225 230 235 240
- Pro Val Ser Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Leu Thr Lys
- Gly Leu Arg Thr His Ile Asp Thr Ile Ile Ala Ser Ala Thr Phe Cys
 260 265 270
- Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Leu Ala Ser 275 280 285
- Gln Val Phe Ile Ile Ser Pro Gln His His Lys Phe Val Gln Asp Cys 290 295 300
- Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala 305 310 315
- (2) INFORMATION FOR SEQ ID NO: 145:
 - (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs



| (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | • |
|---|-----|
| (ii) MOLECULE TYPE: CDNA | |
| (iii) HYPOTHETICAL: NO | |
| (iii) ANTI-SENSE: NO | |
| (ix) FEATURE: (A) NAME/KEY: mat_peptide (B) LOCATION: 2337 | |
| (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 2340 | • |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145: | |
| C TCA ACG GTC ACG GAG AGG GAC ATC AGA ACT GAG GAG TCC ATA TAC Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr 1 5 . 10 | 46 |
| CTT GCT TGC TCT TTA CCC GAG CAG GCA CGG ACT GCC ATA CAC TCA CTG Leu Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu 20 25 30 | 94 |
| ACT GAG AGG CTT TAC GTG GGA GGG CCC ATG CTA AAC AGC AAA GGG CAA Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln 35 40 45 | 142 |
| ACC TGC GGA TAC AGA CGC TGC CGC GCC AGC GGA GTG TTC ACC ACT AGC Thr Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser 50 55 60 | 190 |
| ATG GGA AAT ACC ATC ACG TGC TAC GTG AAG GCA CAA GCA GCC TGT AAG Met Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Gln Ala Ala Cys Lys 65 70 75 | 238 |
| GCT GCG GGC ATA ATT GCC CCC ACG ATG CTG GTG TGC GGC GAC GAT CTA Ala Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu 80 85 90 95 | 286 |
| GTT GTC ATC TCA GAG AGT CAG GGG ACC GAG GAG GAC GAG CGG AAC CTA Val Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn'Leu 100 105 110 | 334 |
| CGA GCC Arg Ala | 340 |

- (2) INFORMATION FOR SEQ ID NO: 146:
 - (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu

1 5 10 15

Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr

Glu Arg Leu Tyr Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln Thr 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met 50 55 60

Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Gln Ala Ala Cys Lys Ala 65 70 75 80

Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asm Leu Arg 100 105 110

Ala

- (2) INFORMATION FOR SEQ ID NO: 147:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (111) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..345
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..342
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

ATG AGC ACA CTT CCT AAA CCA CAA AGA AAA ACC AAA AGA AAC ACC AAC



| Met 1 | Sez | Thr | . Leu | Pro S | Lys | Pr | Gln | λīg | Lys 10 | Thr | Lys | λrg | Asn | Thr 15 | Asn | | |
|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|---|-----|
| Pro | GGC | CAC His | AGG Arg 20 | ACG Thr | TTA Leu | AGT Ser | TCC Ser | CAG GLn 25 | GCG Ala | GCG Ala | GTC Val | AGA Arg | TCG Ser 30 | TTG Leu | GTG Val | | 96 |
| GAG Glu | -uc | ACG Thr 35 | TGC Cys | TAC Tyr | CAC His | GCA Ala | GGG Gly 40 | GCC Ala | CCC | AGT Ser | TGG Trp | GTG Val 45 | TGC Cys | GTG Val | CAG Gla | | 144 |
| TGC Cys | GCA Ala 50 | wid | CIT | CCG Pro | AGC Ser | GGT Gly 55 | CGC Arg | AAC Asn | CTC | GCA Ala | GTA Val 60 | GGC Gly | GCC Ala | AAC Asn | CCA Pro | , | 192 |
| TCC Ser 65 | CCA Pro | GGG Gly | CGC Arg | GCC Ala | GAA Glu 70 | CCG Pro | AGG Arg | GCA Ala | GGT Gly | CCT Pro 75 | GGG Gly | CTC Leu | AGC Ser | CCG Pro | GGT Gly 80 | • | 240 |
| ACC Thr | CTT Leu | GGC Gly | CCC Pro | TAT Tyr 85 | ATG Met | GGA Gly | ATG Met | AGG Arg | GCT Ala 90 | GCG Ala | GGT Gly | GG3 Gly | CAG Gln | GGT Gly 95 | C IÝ | | 288 |
| TCC Ser | TGT Cys | Pro CCC | CGC Arg 100 | GCG Ala | GCT Ala | CTC Leu | Ala | CGT Arg 105 | CGT Arg | GGG Gly | GCC | CAA Gla | ATG Met 110 | ACC Thr | CCC Pro | | 336 |
| GGC | Ala | | | | | | | | | | | | | | | | 345 |

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 amino acids
 - (3) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Pro Gly His Arg Thr Leu Ser Ser Gln Ala Ala Val Arg Ser Leu Val

Glu Phe Thr Cys Tyr His Ala Gly Ala Pro Ser Trp Val Cys Val Gln

Cys Ala Arg Leu Pro Ser Gly Arg Asn Leu Ala Val Gly Ala Asn Pro 50 55 60

Ser Pro Gly Arg Ala Glu Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly 65 70 75 80

Thr Leu Gly Pro Tyr Met Gly Met Arg Ala Ala Gly Gly Gln Gly Gly



95

| | 90 |
|--|----|
| | 40 |

Ser Cys Pro Arg Ala Ala Leu Ala Arg Arg Gly Ala Glm Met Thr Pro 105 100

Gly Ala Gly 115

(2) INFORMATION FOR SEQ ID NO: 149:

85

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..280

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 2..277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

| G GCC TGT GAC CTC AAG GAC GAG GCT AGG AGG GTG ATA ACT TCA CTC Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu 1 5 10 15 | 46 |
|--|-----|
| ACG GAG CGG CTT TAC TGT GGT GGT CCT ATG TTC AAC AGC AAG GGA CAA Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln 20 25 30 | 94 |
| CAC TGC GGT TAC CGC CGC TGC CGT GCT AGT GGG GTG CTA CCC ACC AGC His Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser | 142 |

TTC GGG AAC ACA ATC ACC TGT TAC ATC AAA GCA AAG GCA GCT ACC AAA 190 Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys 55 50

GCT GCC GGA ATT AAA AAT CCA TCA TTC CTT GTC TGC GGA GAT GAC TTG 238 Ala Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu

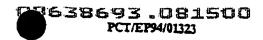
280 GTC GTG ATT GCT GAG AGT GCA GGG ATC GAT GAG GAC AGA GCG Val Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala 85 80

(2) INFORMATION FOR SEQ ID NO: 150:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids



- (B) TYPE: amino acid (D) TOPOLOGY: lin ar
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu Thr
1 5 10 15

Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln His

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe 35 40 45

Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys Ala
50 55 60

Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val 65 70 75 80

Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala 85 90

- (2) INFORMATION FOR SEQ ID NO: 151:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..499
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (E) LOCATION: 1..496
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC AAC
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn

1 5 10 15

CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGC
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly
20
25
30



| | | | CCG Pro | | | | | | | | 144 |
|--|----------------|---|-------------------|---|--|------|-------|---|------|---|-----|
| | | | GAA Glu | | | | | | | | 192 |
| | | | CAG Gln 70 | | | | | | | | 240 |
| | | | TAC Tyr | | | | | | | | 288 |
| | | | GGC Gly | | | | | | | • | 336 |
| | | | AAT Asn | | | | | | | | 384 |
| | | | ATG Met | | | | | | | • | 432 |
| | | | GCT Ala 150 | | | | - | - | | | 480 |
| | TAT Tyr | - | ACA Thr | G | | | | | | | 499 |

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala 35 40 45



| NO 94/ | 2560 | 1 | | | | | | | • | | 0 | | 31 | 36 | 93 PCT/ | . OS. | 1 27 |
|--------|-----------|--------------------|----------------------|---------------------|-------------------------------------|--------------------|----------------------|-------|------|------------|------------|------------|-----|-------------|--------------------|-------|---------|
| | | | | | | | | 20 | 12 | | | | , | | | | |
| Thr | Arg 50 | Lys | Thr | Ser | Glu | Arg 55 | Ser | Gln | Pro | Arg | Gly | Arg | Arg | Gln | Pro | | |
| • | | | | | 70 | | | | | 75 | | | | | Gly 80 | | |
| | | | | 93 | | | | | 90 | | | | | 95 | Trp | | |
| | | | 100 | | | | | 105 | | | | | 110 | | Pro | | |
| Arg | Arg | Lys 115 | Ser | Arg | Asn | Leu | Gly 120 | Lys | Val | Ile | Asp | Thr 125 | Leu | Thr | Cys | | |
| | 770 | | | | | 135 | | | | | 140 | | | | | | |
| Gly (| | | | | 120 | Leu | ALA | His | Gly | Val 155 | Arg | Val | Leu | Gl u | As p 160 | • | |
| Gly ' | Val | Asn | Tyr | Ala 165 | Thr | | | | | | | | | | | | |
| (2) | INFO | RMAT | ION | FOR | SEQ | ID N | C: 1 | 53 : | | | | | | | | | |
| | (i) | (A (B (C |) LE) TY) ST | ngth Pe: Rand | ARAC : 57 nucl EDNE GY: | 9 ba eic S5: | se p acid sing | airs | | | | | | | | ٠ | |
| • | (ii) | MOL | ECUL. | e T Y | PE: | cD:IA | | | | | | | | | | | |
| (i | .ii) | HYP | OTHE | TICA | L: N | 0 | | | | | | | | | | | |
| (i | .ii) | ANT | I-SE | NSE: | NO | | | | | | | | | | | | |
| ` (| ix) | FEA: (A) (B) | NA | ME/K | EY: (| CDS L5 | 79 | | | | | | | | | | |
| (| ix) | FEAT (A) (B) | NA | ME/K | EY: r ON: 1 | na:1 L5 | pept: 76 | ide | | | | | | | | | |
| €. | xi) | SEQU | ENC | E DES | SCRIE | PTIO | 4: SI | EQ 11 | סא כ | : 153 | 3 : | | | | | | |

ACG TGC GGA TTC GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC 48 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly 10 CCC GTT GGG GGC GTC GCA AGG GCT-CTC GCA CAC GGT GTG AGG GTC CTT Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu 20 GAG GAC GGG GTA AAC TAT. CCA ACA GGG AAT TTA CCC GGT TGC TCT TTC



| | | | | | | | | | | | | | | | | • |
|------|------|-----------|-----|-------|-------|------|-----------|-------|-------|------|--------|-----------|--------|-------|------------|-----|
| Glu | Asp | Gly 35 | Val | Asn | īŅī | Pro | Thr 40 | Gly | Asn | Leu | PEO | Gly 45 | Cys | Ser | Phe | |
| | | | | | | - | ~~~ | TCG | *** | CTC: | 300 | GIT | CCG | GCC | TCT | 192 |
| ICI | ATC | TTI | ATT | CTI | 313 | T.Au | Lan | Ser | CAR | Lau | Thr | Val | Pro | Ala | Ser | |
| 261 | 50 | Pae | 116 | Ten | مبہ | 55 | 500 | | O, O | | 60 | | | | | |
| | 30 | | | | | | | | | | | | | | | |
| GCA | GIT | ccc | TAC | CGA | AAT | GCC | TCT | GGG | ATT | TAT | CAI | GII | ACC | AAT | GAT | 240 |
| Ala | Val. | Pro | Tyr | Arg | Asa | Ala | Ser | Gly | Ile | Ty= | His | Val | Thr | Asn | Asp | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| | | | | | | | | | | | | | | | ~~~ | 298 |
| TGC | CCX | AAC | TCT | TCC | ATA | GTC | TAI | GAG | GCA | GAT | AAC | C13 | ATC | CIA | tria | 236 |
| Cys | Pro | Asn | Ser | | Ile | Val | TYT | Glu | 90 | Asp | ASI | FAIT | TTE | 95 | 772 | • |
| | | | | 85 | | | | | 90 | | | | | ,, | | |
| ccn | | COT | 700 | GTG | CCT | TGT | GTC | ATG | ACA | GGT | AAT | GTG | AGT | AGA | TGC | 336 |
| Ala | Bro | Glv | Cve | Val | Pro | Cvs | Val | Met | Thr | Gly | Asn | Val | Ser | Arg | Cys | |
| 77.0 | *-0 | 427 | 100 | | | -3- | | 105 | | • | | | 110 | | | |
| | | | | | | | | | | | | | | | | • |
| TGG | GTC | CAA | ATT | ACC | CCT | ACA | CTG | TCA | GCC | CCG | AGC | cic | GGA | GCA | GTC | 384 |
| Trp | Val | Gla | Ile | Thr | Sio | Thr | | | Ala | Pro | Ser | | | λ.a | Val | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| | | | | - | 3.03 | ~~~ | مسد | | TEC | وشا | ccc | | GGG | GCT | GCC | 432 |
| ACG | GCT | CCT | CTT | 2~4 | AUA | Bla | Val | DAC | TVY | Leu | Ala | Giv | Glv | Ala | Ala | |
| TRE | 130 | | Leu | , Arg | ~-3 | 135 | | | -,- | | 140 | | • | | | • |
| | 130 | | | | | | | | | | | | | | | • |
| CTC | TGC | TCC | GCG | TTA | TAC | GTA | GGA | GAC | GCG | TGT | GGG | GCA | CIA | LIIC | TIG | 480 |
| Leu | Cys | Ser | Ala | Leu | Ty | Val | G13 | / Asp | Ala | Cys | Gly | Ala | Leu | Phe | Leu | |
| 145 | - | | | | 150 | | | | | 155 | | | | | 160 | |
| | | | | | | | , | | | | | | | . ~~ | . 010 | 528 |
| GTA | GGC | CXA | ATC | TTC | : ACC | TAT | AGG | CCI | CGC | CAG | י בייי | . GC. | . AU | - Vai | CAG | |
| Val | Gly | Gla | Met | | | Ty | , Will | l hic | 170 | | |) <u></u> | 2 +44- | 17 | l Glm 5 | • |
| | | | | 165 | • | | | | 1.0 | , | | | | | | |
| 880 | TO | . 220 | TC | TC! | ATT | TAC | AG: | r GGC | : CAI | GT | : ACC | : GG | CAC | C CG | G ATG | 576 |
| Asn | Cvs | . Asi | CVS | Se: | : Ile | Ty | . Se | = G1 | / His | val | Th | - G1 | y His | 5 A. | g Mes | : |
| - 14 | / - | | 180 | | | • | | 189 | 5 | | | | 19 | 0 | | |
| | | | | | | | | | | | | | | | | |
| GCG | ; | | | | | | | | | | | | | | | 579 |
| Ala | ì. | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 20

Glu Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala
130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu 150 155 156

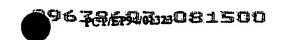
Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met

Ala

(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO .
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..579
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..575



| (xi) | SEQUENCE | DESCRIPTION: | SEQ | ID | NO: | 155: | |
|------|----------|--------------|-----|----|-----|------|--|
|------|----------|--------------|-----|----|-----|------|--|

| ACG | TGC | GGA | TTC | GCC | GAC | CTC | GTG | GGG | TAC | ATC | CCG | ctc | GTA | GGC | GC | 3C | 48 |
|-----------|-----------|------------|------------|-----------|-----------|------------|------------|-----------|-----------|----------|-------|-------|----------|-----------|---------|--------------|-------|
| Thr 1 | Суз | Gly | Phe | Ala S | QZ | Leu | Val | Gly | 10 Lài | Ile | 320 | Leu | Val | Gly 15 | G) | Ly | |
| ccc | GTT | GGG | GGC | GTC | GCA | AGG | GCT | CTC | GCX | CAT | GGT | GTG | AGG | GII | C | TT. | 96 |
| Pro | Val | Gly | G1y 20 | Val | Ala | Arg | Ala | Leu 25 | Aia | A19 | GTÅ | AST | 30 30 | Val | | eu | |
| GAG | GAC | GGG | GTG | AAT | TAT | GCA | ACA | GGG | AAT | CTG | CCT | GGT | TGC | TCT | T | TC he | 144 |
| Glu | Asp | 35 Gly | Val | Asn | TYT | ALA | 40 | GTÅ | ASL | beu | 2.0 | 45 | C/C | - | | | |
| TCT | ATC | TTC | ATT | CIT | GCA | CTT | כזכ | TCG | TGC | CTC | ACT | GTC | CCG | GCC | T | C: | 192 |
| Ser | Ile 50 | Phe | Ile | Leu | Ala | Leu \$5 | Leu | Ser | Cys | Leu | for | Vai | 110 | WIS | . 3 | 4. | • |
| GCA | GTT | ccc | TAC | CGA | AAT | GCC | TCT | GGG | ATC | TAT | CAT | GTC | ACC | AAT | . G | AT. | 240 |
| Ala 65 | Val | Pro | Tyr | Arg | Asn 70 | Ala | Ser | GŢΫ | Ile | 75 75 | H1S | Vai | THE | ASE | | 80 | |
| TGC | CCA | AAC | TCT | TCC | ATA | GTC | TAT | GAG | ಯ | GAT | GAT | CIG | ATC | CT | | iac Ii e | . 288 |
| Cys | Pro | ne.A | Ser | Ser 85 | | Val | Ţŷz | . GI n | 90 | ÇZĀ | ASD | Leu | , TTG | 93 | 5 | 163 | |
| GCA | CCT | GGC | TGC | GTG | cci | TGI | GTC | AGG | | GAT | AAT | GTO | AGT | AG | 3 7 | rgc ~~ | 336. |
| Ala | Pro | Gly | Cys 100 | | . Pro | Cys | va. | 105 | | ASP | ASS | . va. | 110 |) | • | -,- | |
| TGG | GTC | CAP | ATT | ACC | : ccc | : ACC | ; CTC | TO | CCC | CCG | AGC | TT | GGI | A GC | ٦ (| GTC Va: | 384 |
| Trp | Val | Glr 115 | ille | : Thi | Pro |) Thi | 120 | | e Ale | l Pro |) Se: | 12 | 5 | , | _ | | |
| ACC | GC1 | | cm | CGC | ag: | GC: | GT | GA: | T TAC | TIC | GT | G GG | A GG | G GC | T | GCC Ala | 432 |
| Thi | 130 | | Lev | ı Arş | , Ar | 13: | a Va. S | l As; | o Ty: | r Let | 144 | 0 | y GI | y | | 7. 20 | |
| CTC | TG | TC | c GC | TI | A TA | C GT | T GG | A GA | C GC | G TG | r GG | G GC | A CT | A TI | T | TTG Leu | 480 |
| 14 | 5 | | r Ala | | 15 | 0 | | | | 15 | 5 | | | | | 190 | |
| GT | A GG | C CA | A AT | G TT | C AC | C TA | T AG | G CC | T CG | C CA | G CA | T GC | T AC | G GT | rg | CAG Gla | 528 |
| | | | n Me | 16 | 5 | | | | 17 | 0 | | | | • | , 3 | | |
| GA | c TG | C AA | C TG | т тс | C AT | C TA | C AG | T GG | ic ca | C GT | CAC | C G | C C | T C | AG | ATG | 576 |
| As | р Су | s As | n Cy 18 | s Se | r Il | e Ty | r: S€ | 18 | .у на | BV €. | i Tr | i. G. | Ly A. | 90 | | | |
| GC | Α | | | | | | | | | | | | | | | | 579 |
| Al | | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID BO: 156:

Thr. Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu
20 25 20

Glu Asp Gly Val Asn Tyr Ala Thr Gly Asm Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His

Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met

Ala

- (2) INFORMATION FOR SEQ ID NO: 157:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 530 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

| (fii) | HYPOTHETICAL: | NO |
|-------|---------------|----|
| | | |

(iii) ANTI-SENSE: NO

(ix) FEATURE:

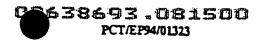
(A) NAME/KEY: CDS
(B) LOCATION: 3..530

(ix) FEATURE:

(A) NAME/KZY: mat_peptide
(B) LOCATION: 3..527

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

| CA CCT ACG ACA GCT CTG CTG GTG GCC CAG TTA CTG CGG ATT CCC CAA Pro Thr Thr Ala Leu Leu Val Ala Gln Leu Leu Arg Ile Pro Gln 1 5 13 | - 47 |
|---|-----------|
| GTG GTC ATT GAC ATC ATC GCA GGG AGC CAC TGG GGG GTC TTG TTT GCT Val Val lie Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala 20 25 30 | 95 |
| GCC GCA TAC TAT GCA TCG GTG GCT AAC TGG ACC AAG GTC GTG CTG GTC Ala Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val 35 40 45 | 143 |
| TTG TTT CTG TTT GCA GGG GTT GAT GCT ACT ACC CAG ATT TCG GGC GGC Leu Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly 50 60 | 191 |
| TCC AGC GCC CAA ACG ACG TAT GGC ATC GCC TCA TTT ATC ACC CGC GGC Ser Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly 65 70 75 | 239 |
| GCG CAG CAG AAA CTG CAG CTC ATA AAT ACC AAC GGA AGC TGG CAC ATT Ala Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile 80 85 90 95 | 287 |
| AAC AGG ACC GCC CTT AAT TGT AAT GAC AGC CTC CAG ACT GGG TTC ATA Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile 100 105 110 | 335 |
| GCC GGC CTC TTC TAC TAC CAT AAG TTC AAC TCT TCT GGA TGC CCG GAT Ala Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp 115 120 125 | 383 |
| CGG ATG GCT AGC TGT AGG GCC CTT GCC ACT TTT GAC CAG GGC TGG GGA Arg Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly 130 135 140 | 431 |
| ACT ATC AGC TAT GCC AAC ATA TCG GGT CCC AGT GAT GAC AAA CCA TAT Thr Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr 145 150 155 | 479 |
| TGC TGG CAC TAT CCC CCA CGG CCG TGC GGA GTG GTG CCA GCC CAA GAG | 527 |



Cys Trp His Tyr Pro Pro Arg Pr Cys Gly Val Val Pro Ala Gln Glu 165 170 175

GTC Val

530

- (2) INFORMATION FOR SEQ ID NO: 158:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 176 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: .linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Pro Thr Thr Ala Leu Leu Val Ala Gln Leu Leu Arg Ile Pro Gln Val

Val Ile Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala Ala 20 25 30

Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val Leu 35 40 45

Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly Ser 50 55 60

Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly Ala 65 70 75 80

Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile Asn 85 90 95

Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile Ala

Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp Arg

Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly Thr 130 135 140

Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr Cys 145 150 155 160

Trp His Tyr Pro Pro Arg Pro Cys Gly Val Val Pro Ala Gln Glu Val 165 170 175

- (2) INFORMATION FOR SEQ ID NO: 159:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

| (D) | TOPOLOGY | : | linea- |
|-----|----------|---|--------|
|-----|----------|---|--------|

(ii) MOLECULE TYPE: cDNA

(iii) HYPCTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS (B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

| C TCG ACC GTT ACC GAA CAT GAC ATA ATG ACC GAA GAG TCC ATT TAC Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr 1 5 10 15 | | | | | | | | | | | | | |
|---|------|--|--|--|--|--|--|--|--|--|--|--|--|
| CAA TCA TGT GAC TTG CAG CCC GAG GCA CGC GCA GCA ATA CGG TCA CTC Gln Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu 20 25 30 | . 94 | | | | | | | | | | | | |
| ACC CAA CGC CTC TAC TGT GGA GGC CCC ATG TAC AAC AGC AAG GGG CAA Thr Gln Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln 35 40 45 | 142 | | | | | | | | | | | | |
| CAG TGT GGT TAT CGC AGA TGC CGC GCC AGC GGC GTT TTC ACC ACC AGT Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser 50 55 60 | 190 | | | | | | | | | | | | |
| ATG GGC AAC ACC ATG ACG TGC TAC ATC AAG GCT TTA GCC TCC TGT AGA Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg 65 70 75 | 238 | | | | | | | | | | | | |
| GCC GCA AGG CTC CGG GAC TGC ACG CTC CTG GTG TGT GGT GAC GAT CTT Ala Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu 80 85 90 95 | 286 | | | | | | | | | | | | |
| GTG GCC ATC TGC GAG AGC CAG GGG ACA CAC GAG GAT GAA GCA AGC CTG Val Ala Ile Cys Glu Ser Glm Gly Thr His Glu Asp Glu Ala Ser Leu 100 105 110 | 334 | | | | | | | | | | | | |
| AGA GCC Arg Ala | 340 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr Gln 1 5 10

Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu Thr

Gln Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met 50 55 60

Gly Asm Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg Ala 65 70 75 80

Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu Arg

Ala

- (2) INFORMATION FOR SEQ ID NO: 161:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..340
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 2..337
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:
- C TCA ACC GCC ACC GAA CAT GAC ATA TTG ACT GAA GAG TCC ATA TAC Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr

46

| | 1 | | | | 5 | | | | | 10 | | | 15 | | | |
|------------------|------------------|--------------------|------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|------------------|--------------------|------------------|------------------|-------------------|------------------|-----|
| CAA Gln | TCA Ser | TGT Cys | GAC Asp | TCG Ser 20 | CAG Gln | CCC | GAC Asp | GCA Ala | CGC Arg 25 | GCA Ala | GCA Ala | ATA | CGG Arg | TCA Ser 30 | CTC Leu | 94 |
| ACC Thr | CAA Gla | CGC Arg | TTG Leu 35 | TTC Phe | TGT Cys | GGA Gly | GGC Gly | CCC PTO 40 | ATG Mes | TAT Tyr | AAC A SE | AGC Ser | AAG Lys 45 | GGG Gly | CAA Gl:: | 142 |
| CŅĀ Gla | igi Cys | GGT Gly 50 | TAT Tyr | Yr3 CGC | AGA Arg | TGC Cys | CGC Arg 55 | GCC Ala | AGC Ser | G17 GCC | GTC Val | TTC Phe 60 | ACC Thr | ACC Thr | AGT Ser | 190 |
| ATG Met | GGC Gly 65 | AAC Asn | ACC Thr | ATG Met | ACG Thr | TGC Cys 70 | TAC Tyr | ATT | AAG Lys | GCT Ala | TTA Leu 75 | GCC Ala | TCC Ser | TGT Cys | AGA Arg | 238 |
| ACC Thr 80 | GCT Ala | G GG Gly | CTC Leu | CGG Arg | GAC Asp 85 | TAC Tyr | ACG Thr | CTC Leu | CTG Leu | GTG Val 90 | TGT Cys | GGT Gly | GAC Asp | GAT Asp | CAT His 95 | 286 |
| GTG Val | GCC Ala | ATC Ile | TGC Cys | GAG Glu 100 | AGC Ser | CAG Glm | GGG Gly | ACA Thr | CAC His 105 | GAG Glu | ÇAT Çek | GAA Glu | GCG Ala | AAC Asn 110 | CTG Leu | 334 |
| AGA . | | | | | | | | | | | | | | | | 340 |

(2) INFORMATION FOR SEQ ID NO: 162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

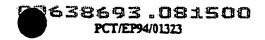
Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr Gln
1 5 10 15

Ser Cys Asp Ser Gln Pro Asp Ala Arg Ala Ala Ile Arg Ser Leu Thr
20 25 30
Gln Arg Leu Phe Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln
35

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met

Gly Asn Thr Met Thr Cys Tyr Ile-Lys Ala Leu Ala Ser Cys Arg Thr
65 70 75 80

Ala Gly Leu Arg Asp Tyr Thr Leu Leu Val Cys Gly Asp Asp His Val 85 90 95



| Ala | 11 | Cys | Glu | Ser | Gla | Gly | Thr | His | Glu | Asp | Glu | Ala | Asn | Lau | Ara |
|-----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | | | 100 | | | | | 105 | | - | | | 110 | | , |

Ala

| (2) | INFORMATION | FCR | SEO | TD | MO. | :63. |
|-----|-------------|-----|-----|----|-----|------|
| | | | | | | |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear.
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..499

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

| ATG Met 1 | AGC Ser | ACG Thr | AAT Asn | CCT Pro S | AAA Lys | CTT Leu | CAA Gln | aga Azg | AAA Lys 10 | ACC Thr | AAA Lys | CGT | AAC Asn | ACC Thr 15 | AAC Asn | 48 |
|------------------|------------|------------------|------------------|------------------|------------------|------------|------------------|------------------|------------------|------------------|------------|------------------|------------------|------------------|------------------|-----|
| CGC Arg | CGC | CCC Pro | ATG Met 20 | GAC Asp | GTT Val | AAG Lys | TTC Phe | CCG Pro 25 | GGT Gly | GGT Gly | GGC Gly | CAG Gln | ATC Ile 30 | GTT Val | GGC Gly | 96 |
| GGA Gly | GTT Val | TAC Tyr 35 | TTG Leu | TTG Leu | CCG Pro | CGC | AGG Arg 40 | GGC Gly | CCT Pro | AGG Arg | TTG Leu | GGT Gly 45 | GTG Val | CGC | GCG Ala | 144 |
| | | | ACT Thr | | | | | | | | | | | | | 192 |
| ATC Ile 65 | Pro | AAG Lys | GCG Ala | CGC | CGA Arg 70 | TCC Ser | GAG Glu | GGC Gly | AGA Arg | TCC Ser 75 | Trp | GCG Ala | CAG Gln | Pro CCC | GGG Gly 80 | 240 |
| TAT Tyr | CCT Pro | TGG Trp | CCC Pro | CTT Leu 85 | TAC Tyr | GGC Gly | AAT Asn | -GAG Glu | GGC Gly 90 | TGT Cys | GGG Gly | TGG Trp | GCA Ala | GGG Gly 95 | Ità Lee | 298 |
| CTC | CTG | TCC | CCT | CGC | GGG | TCT | CGG | CCG | TCT | TGG | GGC | CCT | AAT | GAT | ccc | 336 |



| Leu | Leu | Ser | Pro 100 | Arg | Gly | Ser | Arg | PT0 105 | Ser | Izp | Gly | PE | Asn 110 | Asp | Pro | | |
|-----|-----|-----|------------|-------------------|-------------------|-----|-----|------------|-----|-----|-----|----|------------|-----|-----|---|-----|
| | | | | | AAC Asn | | | | | | | | | | | 3 | 84 |
| | | | | | ATG Met | | | | | | | | | | | 4 | 132 |
| | | | | | GCC Ala 150 | | | | | | | - | | | | 4 | 180 |
| | | | | GCA Ala 165 | ACA Thr | G | | | | | | | | | | 4 | 199 |

- (2) INFORMATION FOR SEQ ID NO: 164:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (3) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Met Ser Thr Asn Pro Lys Leu Gln Arg Lys Thr Lys Arg Asn Thr Asn 1 5 10 15

Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50 60

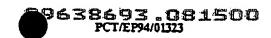
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
100 105 110

Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys
115 120 - 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val 130 135 140



Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp 145 150 155 160

Gly Ile Asn Tyr Ala Thr 165

(2) INFORMATION FOR SEQ ID NC: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDMESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

| ATGAGCACGA | ATCCTAAACC | TCAAAGAAAA | ACCAAACGTA | ACACCAACCS | CCGCCCTATG | 60 |
|------------|------------|------------|------------|------------|--------------|-----|
| GACGTTAAGT | TCCCAGGCGG | TGGTCAGATC | GTTGGCGGAG | TTTACTTGTT | GCCGCGCAGG | 120 |
| GGCCCCAGGT | TGGGTGTGCG | CGCGACTCGG | AAGACTTCGG | AGCGGTCGCA | ACCTCGTGGG . | 180 |
| AGGEGECAAC | CTATCCCCAA | GGCGCGCCGA | ACCGAGGGCA | GATCCTGGGC | GCAGCCCGGG | 240 |
| TATCCTTGGC | CCCTTTACGG | CAATGAGGGC | TGTGGGTGGG | CAGGGTGGCT | CCTGTCCCCT | 300 |
| CGCGGNTCTC | GGNCGTCTTG | GGGCCCCAAT | GATCCCCGGN | GGAGATCCCG | CAACTTGGGT | 360 |
| AAGGTCATCG | ATACCCTAAC | ATGCGGCTTC | GCCGACCTCA | TGGGATACAT | CCCGCTTGTA | 420 |
| GCCCCCCC | TGGGTGGCGT | CGCCAGGGCC | CTGGCACATG | GTGTTAGGGC | TGTGGAAGAC | 480 |
| GGGATCAATT | ATGCAACAG | | | | | 499 |

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn

| | | | | | | 215 | | • | | | | | | | _ |
|------------------------|---------------------------------------|-------------------------|---------------------|-------------|-----------------------|------------|------------|-----------|-----------|-----------|------------|------------|------------|-----------|----|
| 1 | | | 5 | | | | | 10 | | | | | 15 | | |
| Arg | Arg Pro | Me: 20 | Asp | Val | Lys | Phe | Pro 25 | Gly | Gly | Gly | Gln | Ile 30 | Val | Gly | |
| Gly | Val Tyr 35 | Leu | Leu | Pro | Arg | Arg 40 | Gly | Pro | Arg | Leu | Gly 45 | Val | Arg | Ala | |
| Thr | Arg Lys | Thr | Ser | Glu | Arg 55 | Ser | Gla | Pro | Arg | Gly 60 | Arg | Arg | Gln | Pro | |
| Ile 65 | Pro Lys | Ala | Arg | Arg 70 | Thr | Glu | Gly | Arg | Ser 75 | Trp | Ala | Gla | Pro | Gly 80 | |
| ŢŶī | Pro Trp | | Leu 85 | īyr | Gly | Asn | Glu | Gly 90 | Cys | Gly | Įzp | Ala | Gly 95 | ŢŢ | |
| Leu | Leu Ser | Pro 100 | Arg | Xaá | Ser | Azg | Xaa 105 | Ser | Lrp | Gly | Pro | Asn 110 | Asp | Pic | |
| Arg | Xaa Arg 115 | Ser | Arg | Asn | Leu | Gly 120 | Lys | Val | Ile | Asp | Thr 125 | Гел | | | |
| (2) INFO | RMATION : | FOR S | EQ I | D NO |): 16 | 7: | | | | | | | | | |
| (i) | SEQUENCE (A) LEE (B) TY (C) ST (D) TO | ngth: Pe: n Rande | 579 ucle DNES | bas ic a | se pa cid singl | irs | | | | | | | | | |
| (ii) | MOLECUL | E TYP | E: c | :DNA | | | | | | | | | | | |
| (iii) | HYPOTHE | TICAL | : NO | • | | | | | | | | | | | |
| (iii) | ANTI-SE | NSE : | NO | | | | | | | | | | | | |
| (ix) | FEATURE (A) NAI (B) LO | ME/KE | | | 79 | | | | | | | | | | |
| (ix) | FEATURE (A) NAI (B) LO | ME/KE | | _ | • | de | | | | | | | | | |
| (xi) | SEQUENC | E DES | CRIP | TION | : SE | II Q | NO: | 16 | 7: | | | | • | | |
| ACA TGC (Thr Cys (| | | | | | | | | | | | | | | 49 |
| CCC GTG C Pro Val C | GT GGC (| GTC G Val A | CC A la A | rea y | CC-C | TG C | SCA (| CAT (| GGT (| STT : | AGG (| GCT Ala | GTG Val | | 96 |

GAA GAC GGG ATC AAT TAT GCA ACA GGG AAC CTT CCC GGT TGC TCC TTT

30

144

20



| Glu | Asp | Gly 35 | Ile | Asn | Tyr | Ala | Thr 40 | Gly | Asn | Leu | Pro | Gly 45 | Суз | Ser | Phe | |
|-----|-----|-----------|-----|-----|-----|------------------|-----------|-----|-----|-----|------|-----------|-------|-----|-----|-------|
| TCT | ATC | TTC | CTC | TTG | GCG | CTC | CIC | TCG | TGC | CTG | ACT | GTT | CCC | ACA | TCG | 192 |
| Ser | Ile | Phe | Leu | Leu | Ala | Leu | Leu | Ser | Cys | Leu | Thr | Val | Pro | Thr | Ser | 494 |
| | 50 | | | | | 55 | | | • | | 60 | | | | - | |
| GCC | GTT | AAC | 727 | CGC | AAT | GCT | TCG | GGC | ATT | TAT | CAC | ATC | AC2 | AAT | GAC | 240 |
| Ala | Val | Asn | Tyr | Arg | Asn | Ala | Sez | Gly | Ile | Tyr | His | Ile | Thr | Asn | Asp | |
| 63 | | | | | 70 | | | | | 75 | | | | | 80 | |
| TGC | CCG | AAT | GCA | AGC | ATA | GTG | TAC | GAG | ACC | GAA | AAT | CAC | ATC | TTA | CAC | 288 |
| Cys | Pro | Asn | Ala | Ser | Ile | Val | Tyr | Glu | Thr | Glu | Asn | His | Ile | Leu | His | |
| | | | | 85 | • | | | | 90 | | | | | 95 | | |
| CTC | CCA | GGG | TGC | GTA | CCC | TGT | GTG | AGG | ACT | GGG | AAC | CAG | TCG | CGG | TGT | 336 |
| Leu | Pro | Gly | Cys | Val | Pro | C _y s | Val | Arg | Thr | Gly | Asn | Gln | Ser | Arg | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | • |
| TGG | GTG | GCC | CTC | ACT | ccc | ACA | GTA | GCG | TCG | CC3 | The | 000 | | | 000 | 204 |
| Trp | Val | Ala | Leu | Thr | 520 | Thr | Val | Ala | Ser | Pro | Tyr | 212 | GIV | NI- | 0-0 | 384 |
| • | | 115 | | | | | 120 | | | | -7- | 125 | 417 | ~~ | FLU | |
| CTT | GAG | ccc | TTG | CGG | CGT | CAT | GTG | GAC | CTG | ATG | GTA. | COT | ترجية | ccc | 300 | 432 |
| Leu | Glu | Pro | Leu | Arg | Arg | His | Val | GZA | Leu | Mes | Val | Glv | 212 | Δia | アトー | . 432 |
| | 130 | | | _ | _ | 135 | | • | | | 140 | , | | | | |
| | | | | | | | • | | | | | | | | | |
| ATG | TGT | TCC | GCC | CIC | TAC | ATC | GGC | GAC | TTG | TGC | GGT | GGC | TTA | TTC | TTG | 480 |
| 145 | Cys | ser | ALA | Leu | Tyr | Ile | GīÀ | ζεκ | Leu | | Gly | Gly | Leu | Phe | | |
| 743 | | | | | 150 | | | | | 155 | | | | | 160 | |
| GTG | GGC | CAA | ATG | TTC | ACC | TTC | حمع | CCG | CGA | CGT | CAC | TGG | ACC | ACT | CAG | 528 |
| Val | Gly | Gln | Met | Phe | Thr | Phe | Gln | Pro | Arq | Ara | His | Tro | The | Thr | Glm | 3.0 |
| | | | | 165 | | | | | 170 | - | | • | | 175 | | |
| GAC | TGC | AAT | TGT | TCC | ATC | TAC | ACG | GGC | CAC | ATT | ACG | GGT | CAT | CGG | ATG | 576 |
| Asp | Cys | Asn | Cys | Ser | Ile | Tyr | Thr | Gly | Bis | Ile | Thr | Gly | His | Arg | Met | 2.0 |
| | | | 180 | | | | | 185 | | | | • | 190 | - | | |
| GCA | | | | | | | | | | | | | | | | 579 |
| Ala | | | | | | | | | | | | | | | | 3/3 |

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1 5 10 15



Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys S r Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser 50 55 60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys 100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro 115 120 125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 140

Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Pha Leu 145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..579
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..576

| (xi) | SEQUENCE | DESCRIPTION: | SEQ | ID | NO: | 169; |
|------|----------|--------------|-----|----|-----|------|
|------|----------|--------------|-----|----|-----|------|

| AC | TGC | GGG | TIC | GCC | . GYC | CTC | ATG | GGA | TAC | ATO | : cc | CIT | GTA | GGC | GCC | 48 |
|-----|-------------|-------------|------------|-------|------------|------------|-----|------|-----|-------------|------|------|------|------|--------------|-------|
| | 3- | 3 G13 | Phe | : WTG | ASP | Leu | Met | Gly | Ty: | Ile | Pro | Leu | Val | G1v | Ala | 40 |
| 1 | • | | | 5 | j | | | | 10 | ١. | | | | 15 | | |
| | GTO | | | | | | | | | | | | | | | |
| P=: | Val | GIV | GO. | . Gic | ala | AGA | GCC | CTG | GCA | CXC | GGT | GI | AGG | GCT | GTG | 96 |
| | | | 20 | AGT | ALG | wig | wid | Leu | Ata | His | Gly | Val | Arg | Ala | Val | |
| | | | | | | | | 25 | | | | | 30 | | | |
| GAA | GAC | GGG | ATC | AAC | TAC | GCA | ACA | GGG | 227 | | | | 700 | | TTT | |
| Glu | Asp | Gly | Ile | Asn | Ty | Ala | The | Glv | Asa | Lev | 250 | Giv | 700 | FOC | Phe | 144 |
| | | 35 | | | | | 40 | • | | | | 45 | Cia | 367 | FIIE | |
| | | | | | | | | | | | • | | | | | |
| TCT | ATC | TIC | CIC | TIG | GCX | CII | CIC | TCG | TGC | CTC | ACT | GTT | CCC | GCG | TCG | 192 |
| ser | 176 | Pitte | Leu | Leu | Ala | Lau | Leu | Ser | Cys | Leu | The | .Val | Pro | Aia | Ser | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| GGC | GTT | 220 | TAT | cac | A 3.T | CCT | T | | | | | | | | | |
| Gly | Val | Asn | Tvr | Ara | VVI. | GCT | CAT | Clar | GIT | TAT | CYC | YIC | ACC | AAC | GAÇ | 240 |
| 65 | - | | -,- | , | 70 | Ala | 367 | GIY | Val | | HIS | Ile | Thr | Asn | | |
| | | | | | | | | | | 75 | | | | | 80 | |
| TGC | CCG | AAT | GCG | AGC | ATA | GTG | TAC | GAG | ACC | GAC | ALT | CZC | 377 | | C3.C | . 200 |
| Cys | Pro | Asn | Ala | Ser | Ile | Val | Tyr | Glu | Thr | Asp | Asc | His | Tie | 7.00 | Wie | . 288 |
| | | | | 85 | | | - | | 90 | | | | | 95 | 44.0 | |
| | | | | | | | | | | | | | | | | |
| CIC | CCA | GGG | TGC | GTA | CCC | TGT | GTG | AAG | ACC | GGG | AAC | CAG | TCG | CGG | TGT | 336 |
| reu | Pro | GIA | Cys | Val | Dio | Cys | Val | Lys | The | Gly | Asn | Glm | Ser | Arg | Суз | |
| | | | 100 | | | | | 105 | | | | | 110 | | - | |
| TGG | GTG | GCC | CTC | ACT | ccc | 3.63 | | ~~~ | | | | | | | | |
| Trp | Val | Ala | Leu | Thr | Pro | ACA Thr | Val | 813 | TCG | CCT | TAC | GTC | GGT | GCT | CCG | 384 |
| • | | 115 | | •••• | | ***- | 120 | wa | Ser | PTO | TYT | | GIY | Ala | Pro | |
| | | | | | | | | | | | | 125 | | | | |
| CTC | GAG | CCC | TTG | CGG | CGC | CAT | GTG | GAC | CIG | ATG | GTA | GGT | GCT | GCC | ACC | 432 |
| Leu | Glu | Pro | Leu | Arg | Arg | His | Val | Asp | Leu | Met | Val | Glv | Ala | Ala | Thr | 432 |
| | 130 | | | | | 135 | | | | | 140 | • | | | | |
| GTC | T CC | m 00 | | | | | | | | | | • | | | | |
| Val | 700 | 100 | GCC Bla | CIC | TAC | GIC | GGC | GAC | CIG | TGC | GGT | GGC | TTA | TTC | TTG · | 480 |
| 145 | -ys | 361 | WIG | ren | 19E | val | GTĀ | ASD | Leu | | Gly | Gly | Leu | Phe | Leu | • |
| | | | | | 130 | | | | | 155 | | | | | 160 | |
| GTA | GGC | CAA | ATG | TTC | ACC | TTC | CAA | cca | CGZ | CCC | CAC | TCC | 200 | 100 | ~~~ | |
| Val | Gly | Gln | Met | Phe | Thr | Phe | Gla | Pro | Aza | Ara | Hie | L | The | Th- | CAG | 528 |
| | | | | 165 | | | | | 170 | 3 | | ••• | **** | 175 | G1 11 | |
| | | | | | | | | | | | | | | | • | |
| GAC | TGT | AAT | TGT | TÇC | ATC | TAC | GCA | GGG | CAT | ATT | ACG | GGC | CAT | CGG | ATG | 576 |
| Asp | Cys | Asn | Cys | Ser | Ile | Tyr | Ala | Gly | His | Ile | Thr | Gly | His | Arg | Met | |
| | | | 180 | | | | | 185 | | | | | 190 | - | | |
| GCT | | | | | | | | | | | | | | | | ٠ |
| Ala | | | | | | | | | | | | | | | | 579 |
| | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 170:



- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala Ris Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Gly Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Asp Asn His Ile Leu His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys
100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Val Gly Ala Pro 115 120 125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 140

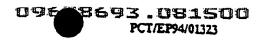
Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu 145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met 180 185 190

Ala

- (2) INFORMATION FOR SEQ ID NO: 171:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid(C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA



| (iii) | HYPOTHETICAL: | NO |
|-------|---------------|----|
|-------|---------------|----|

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: OS

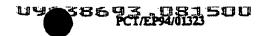
(B) LOCATION: 1..579

(ix) FEATURE:

(A) NAME/KEY: mat_peptide (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

| | | | | | | | | _ | | - | . • • | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| ACA Thr | Cys | GGC Gly | TTC Phe | GCC Ala 5 | Asp | CTC | ATG Met | GGA Gly | TAC Tyr 10 | Ile | CCG Pro | CTT | GTG 'Val | GGC Gly 15 | GCC Ala | 48 |
| Pro | GTT Val | Gly | GGC Gly 20 | GTC Val | GCC Ala | AGA | GCC Ala | CTT Leu , 25 | λla | CAC | GCC | GTC Val | AGG Arg 30 | GCT Ala | GTG Val | 96 |
| GAA Glu | GAC Asp | GGG Gly 35 | ATT | AAC Asn | TAT Tyr | GCA Ala | ACA Thr 40 | GGG Gly | AAC Asn | CTT | CCT Pro | GGT Gly 45 | TGC Cys | TCC Ser | TTT Phe | 144 |
| TCT Ser | ATC Ile 50 | Pne | CTT | CTG Leu | GCA Ala | CTT Leu 55 | CTC | TCG | TGC Cys | CTG | ACT Thr 60 | GTC Val | CCC | GCC Ala | TCG Ser | 192 |
| GCT Ala 65 | GTG Val | CAT His | TAT Tyr | CAC His | AAC Asn 70 | ACC Thr | TCG Ser | GGC Gly | ATC Ile | TAC Tyr 75 | CAC His | CTC Leu | ACC Thr | AAT Asn | GAC Asp 80 | 240 |
| TGC Cys | Pro | AAC Asn | TCT Ser | AGC Ser 85 | ATA Ile | GTC Val | TTT Phe | GAG Glu | GCA Ala 90 | GTC Val | CAT His | CYC | ATC Ile | TTG Leu 95 | CAC His | 298 |
| CTT Leu | CCA Pro | GGA Gly | TGC Cys 100 | GTC Val | CCT Pro | TGT Cys | GTA Val | AGA Arg 105 | ACT Thr | GGG Gly | AAC Asd | CAG Gln | TCT Ser 110 | CGG Arg | TGC Cys | 336 |
| TGG Trp | GTA Val | GCC Ala 115 | TTG Leu | ACC Thr | CCC | ACG Thr | CTG Leu 120 | GCC Ala | GCG Ala | CCY CCY | TAC Tyr | CTT Leu 125 | GGC Gly | GCT Ala | CCA Pro | .384 |
| CTC Leu | GAG Glu 130 | TCC Ser | ATG Met | CGG Arg | CGT Arg | CAC His 135 | GTG Val | GAT Asp | TTG Leu | ATG Met | GTG Val 140 | GGC Gly | ACT Thr | GCT Ala | AĊA Thr | 432 |
| TTG Leu 145 | TGC Cys | TCA Ser | GCA Ala | Leu | TAC Tyr 150 | GTT Val | ejà eee | GAC Asp | CTG Leu | TGC Cys 155 | GGG Gly | GGC Gly | ATA Ile | TTC Phe | CTA Leu 160 | 430 |
| GCG Ala | GGC Gly | CAG Gln | ATG Met | TTC Phe 165 | ACC Thr | TTC Phe | CGG Arg | Pro CCC | CGC Arg 170 | CTC Leu | CAT His | TGG Trp | ACC Thr | ACC Thr 175 | CAG Gln | 528 |



| | | Cys 180 | | | | | | | 576 |
|----|-----|------------|--|--|--|--|--|--|-----|
| GC | 3 | | | | | | | | 579 |
| Al | a . | | | | | | | | |

- (2) INFORMATION FOR SEQ ID NO: 172:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Leu Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Val His His Ile Leu His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys
100 105 110

Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro Tyr Leu Gly Ala Pro 115 120 125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ile Phe Leu 145 150 155 160

Ala Gly Gln Met Phe Thr Phe Arg Pro Arg Leu His Trp Thr Thr Gln 165 170 175

Glu Cys Asn Cys Ser Thr Tyr Pro Gly His Ile Thr Gly His Arg Met 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 173:

| (i) | SEQUENCE | CHARACTERISTICS |
|-----|----------|-----------------|
| | | |

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CONA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

| ACG Thr 1 | TGC Cys | GGT Gly | TCC Ser | GCC Ala 5 | gac Asp | CTC | ATG Met | GGA Gly | TAC Tyr 10 | ATC Ile | CCG Pro | CTC Leu | GTA Val | GGC Gly 13 | GCC Ala | 48 |
|-----------------|------------|------------------|-------------------|------------------|------------|------------|------------------|-------------------|------------------|------------|------------|------------------|-------------------|------------------|------------|-----|
| Pro | GTG Val | GGT Gly | GGC Gly 20 | GTC Val | GCC Ala | AGG Arg | GCC Ala | TTG Leu 25 | GCG Ala | CAT His | GGC Gly | GTC Val | AGG Arg 30 | GCT Ala | GTG Val | 96 |
| GAG Glu | GAC Asp | GGG Gly 35 | ATA Ile | AAC Asn | TAT Tyr | GCA Ala | ACA Thr 40 | GGG Gly | AAC Asn | CTT Leu | CCT Pro | GGT Gly 45 | TGC Cys | TCT Ser | TTT Phe | 144 |
| | | | | CTG Leu | | | | | | | | | | | TCA Ser | 192 |
| | | | | CAC His | | | | | | | | | | | | 240 |
| | | | | AGC Ser 85 | | | | | | | | | | | | 298 |
| CTT Leu | CCA Pro | GGA Gly | TGC Cys 100 | GTC Val | CCC | TGT Cys | GTG Val | AGA Arg 105 | ACT Thr | GGG Gly | AAC Asn | CAG Gln | TCA Ser 110 | CGA Arg | TGC Cys | 336 |
| | | | | | | | | | | | | | | | CCA Pro | 384 |

120

125

| | | | | | | | | | | | | 44.7 | | | | | |
|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|---|-----|
| CTT Leu | GAG Glu 130 | TCC Ser | ATG Met | CGA | CGT Arg | CAT His 135 | GTG Val | GAT Asp | TTG Leu | ATG Met | GTA Val 140 | GGC Gly | ACT Thr | GCC Ala | ACA Thr | | 432 |
| TTG Leu 145 | TGC Cys | TCC Ser | GCA Ala | CTC Leu | TAC Tyr 150 | ATT Ile | GGA Gly | GAT ÇEK | CTG | 122 Càa 10C | GGA Gly | GGC Gly | ATA Ile | TTT Phe | CTA Leu 160 | | 480 |
| GTG Val | GGC Gly | CAG Gla | ATG Met | TTC Phe 165 | AAC Asn | TTC Phe | AGG Arg | CCC | CGC Arg 170 | Tes CIG | OAC elE | Lrb Lec | ACC Thr | ACC Thr 175 | CAG Gln | | 528 |
| GAG Glu | TGC Cys | TAA neA | TGT Cys 180 | TCC Ser | ATC Ile | TAT Tyr | CCA Pro | GGC Gly 185 | HTS | ATC Ile | ACG Thr | GGT Gly | CAC His 190 | AGA Arg | ATG Met | | 576 |
| GCG Ala | | | | | | | | | | | | | | | | • | 579 |

- (2) INFORMATION FOR SEQ ID NO: 174:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Thr Cys Gly Ser Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Glu His His Ile Leu His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys
100 105 110

Trp Ile Ala Leu Thr Pro Thr Leu Ala Ala Pro His Ile Gly Ala Pro 115 120 125

| VO 94/25601 | | • | | U | | B | 69 | PCT/EP94/01323 |
|------------------------------------|------------|----------------|----------------|------------|-----|------------|------------|----------------|
| | | 22 | 4 | | | | | |
| Leu Glu Ser Met Arg Arg 130 | His 135 | Val Asp | Leu Met | Val 140 | Gly | Thr | Ala | Thr |
| Leu Cys Ser Ala Leu Tyr 145 150 | Ile | Gly Asp | Leu Cys | | Gly | Ile | Phe | Leu 160 |
| Val Gly Gln Met Phe Asn 165 | Phe . | Arg Pro | arg Leu 170 | His | Trp | Thr | Thr 175 | Gln |
| Glu Cys Asn Cys Ser Ile 180 | Tyr | Pro Gly 185 | His Ile | Thr | Gly | His 190 | Arg | Met |
| Ala | | | | | | | | |
| | | | | | | | | |
| (2) INFORMATION FOR SEQ | ID N | 0: 175: | | | | | | |
| (1) SEQUENCE CHARA | CTERI | STICS: | | | | | | |
| (A) LENGTH: S | 79 ba | se pair: | 3 | | | | | - |
| (B) TYPE: nuc | | | | | | | | |
| (C) STRANDEDN | | | | | | | • | |
| (D) TOPOLOGY: | line | ar | | | | | | |
| (ii) MOLECULE TYPE: | CDNA | | | | | | | |
| (iii) HYPOTHETICAL: | NO | | | | | | | • |
| (iii) ANTI-SENSE: NO | | | | | | | | |
| (ix) FEATURE: | | | • | | | | | |
| (A) NAME/KEY: | | | | | | | | |
| (B) LOCATION: | 157 | 79 | | | | | | |
| (ix) FEATURE: | | | | | | | | |
| (A) NAME/KEY: (B) LOCATION: | 151 | peptide 76 | | | | | | |
| (xi) SEQUENCE DESCR. | | | | | | | | |
| ACG TGC GGC TTT GCC GAC | CTC F | ATG GGA | TAC ATC | CCG | CTC | GTG | GGC | GCC 4: |
| Thr Cys Gly Phe Ala Asp | Leu N | Met Gly | Tyr Ile | Pro | Leu | Val | Gly | Ala |
| | | | | | | | • • | |

| ACG | TGC | GGC | TIT | GCC | GAC | CTC | ATG | GGA | TAC | ATC | CCG | CTC | GTG | GGC | GCC | 48 |
|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Cys | Gly | Phe | Ala | Asp | Leu | Met | Gly | Tyr | Ile | Pro | Leu | Val | Glv | Ala | |
| 1 | | | | 5 | | | | • | 10 | | | | | 15 | | |
| | | | | | | | | | | | | | | | | |
| CCT | GTG | GGT | GGÇ | GTC | GCC | AGG | GCC | TTG | GCX | CAT | GGT | GTC | AGG | GCC | GTG | 96 |
| Pro | Val | Gly | Gly | Val | Ala | Arg | Ala | Leu | Ala | His | Gly | Val | Arg | Ala | Val | |
| | | | 20 | | | | | 25 | | | - | | 30 | | | |
| | | | | | | | | | | | | | | | | |
| GAG | GAC | GGG | ATT | AAC | TAT | GCA | ACA | GGG | AAT | CTT | CCC | GGT | TGC | TCC | TIT | 144 |
| Glu | Asp | Gly | Ile | Asn | Tyr | Ala | Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | |
| | | 35 | | | | | 40 | | | | | 45 | _ | | | |
| TCT | ATC | TTC | CTT | CTA | GCA | CTT | CTC | TCG | TGC | TTG | ACT | GTC | CCG | GCC | TCG | 192 |
| Ser | Ile | Phe | Leu | Leu | Ala | Leu | Leu: | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | |
| | 50 | | | | | 55 | | | - | | 60 | | | | | |
| | | | | | | • | | | | | | | | | | |
| GCG | CAG | CXC | TAC | CGG | AAC | ATC | TCG | GGC | ATT | TAT | CAC | GTC | ACC | AAT | GAC | 240 |
| Ala | Gln | His | Tyr | Arg | Asn | Ile | Ser | Gly | Ile | Tyr | His | Val | Thr | Asn | Asp | |

385474831500

| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
|-----|-----|-----|-----|-----------|------|-----|-----|-----|-----------|-----|-----|-----|------------|-----------|------|-------|
| TGC | CCG | AAC | TCT | AGT | ATA | GTG | TAT | GAA | GCT | GAC | CAT | CAT | ATC | ATG | CAT | 288 |
| Cys | Pro | Asn | Ser | Ser 85 | Ile | Val | Tyr | Glu | Ala 90 | Yzb | His | His | Ile | Met 95 | His | • |
| دښې | CCI | 000 | ~~ | | ~~ | | | | | | | | | | | |
| Len | D-0 | Glu | TGT | 11-1 | Bro. | 100 | 610 | AGA | ACC | GGG | AAC | ACC | TCG | CGC | TGC | 336 |
| | *.0 | GIY | 100 | AGI | F13 | cys | AST | 105 | TRE | GTÅ | asn | Thr | Ser 110 | Arg | Civa | |
| TGG | GTT | cci | TTA | ACA | CCC | ACT | GTG | GCT | GCC | ccc | TAT | GTT | GGC | GCG | CCS | 384 |
| Try | Val | Pro | Leu | Thr | Pro | The | Val | Ala | Ala | 520 | Tyr | Val | Gly | Ala | Pro | 304 |
| | | 115 | | | | | 120 | | | | • | 125 | | | - | |
| CTÇ | GAA | TCC | ATG | CGG | CGG | CAC | GTG | GAC | TTA | ATG | GTG | GGT | GCC | GCC | ACC | 432 |
| Leu | Glu | Ser | Met | λrg | yra | His | Val | Asp | Leu | Met | Val | Gly | Ala | Ala | Thr | • |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| GTC | TGC | TCG | GCC | CIG | TAC | ATC | GGA | GAC | CII | TGC | GGA | GGT | GTC | TTC | CTG | - 480 |
| Val | Cys | Ser | Ala | Leu | Iyr | Ile | Gly | Asp | Leu | Cys | Gly | Gly | Val | Phe | Leu | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| GTC | GGG | CAG | ATG | TTC | ACC | TTC | CGG | CCG | CGC | CGC | CAT | TGG | ACT | ACC | CAG | 528 |
| Va! | Gly | Gln | Met | Phe | The | Phe | Arg | Pro | Arg | λrg | His | Trp | Thr | Thr | Gl= | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| GAC | TGC | AAC | TGC | TCT | ATC | TAT | GAT | GGC | CAC | ATC | ACC | GGC | CAT | AGA | ATG | 576 |
| Asp | Cvs | Asn | Cys | Ser | Ile | Tyr | Asp | Gly | His | Ile | Thr | Gly | His | Arg | Met | |
| | | | 180 | | | ٠. | | 185 | | | | | 190 | | | |
| GCT | | | | | | | | | | | | | | | | 579 |
| Ala | | | | | | | | | | | | | | | | 373 |

(2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

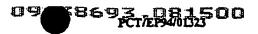
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 5 10 15 ...

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

Ser Ile Phe.Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60



Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pr Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His
'85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys
100 105 110

Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro 115 120 125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 155 160

Val Gly Gln Mer Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg Met 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
 (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..579
- (ix) FEATURE:
 - (A) NAME/KEY: mat peptide
 - (B) LOCATION: 1..576

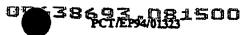
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ACG TGC GGG TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCT

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 5 10 15

Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val



576

579

| | | 227 | | |
|-----------------|---------------|-----------------|-----------------|-------------|
| 20 | | 25 | 30 | |
| GAG GAC GGG ATC | AAT TAC GCA | ACA GGG AAC CTT | CCC GGC TGC TCC | TTT 144 |
| | | | Pro Gly Cys Ser | |
| 35 | | 40 | 45 | |
| | | | ACT GTC CCA GCG | |
| Ser Ile Phe Leu | Leu Val Leu I | Leu Ser Arg Leu | Thr Val Pro Ala | Ser |
| 50 | 55· | | 60 | |
| GCT CAG CAC TAC | CGG AAT GCA 1 | TCG GGC ATC TAC | CAT GTC ACC AAC | GAC 240 |
| Ala Gla His Tyr | Arg Asn Ala S | Ser Gly Ile Tyr | His Val Thr Asn | Q2 K |
| 65 | 70 | 75 | | 80 |
| TGC CCG AAC TCC | AGT ATT GTG 1 | TAT GAA GCC GAC | CAT CAC ATC ATG | CAC 288 |
| Cys Pro Asn Ser | Ser Ile Val 1 | Tyr Glu Ala Asp | His His Ile Met | His |
| | 85 | 90 | 95 | |
| CTA CCC GGG TGT | GTG CCC TGT C | STA AGA ACT GGG | AAT GTC TCG CGT | TGC 336 |
| Leu Pro Gly Cys | Val Pro Cys \ | Val Arg Thr Gly | Asn Val Ser Arg | Cys |
| 100 | | 105 | 110 | |
| TGG ATT CCT TTA | ACA CCC ACT C | STA GCC GTC CCC | TAC CTC GGG GCT | CCA 384 |
| Trp Ile Pro Leu | The Pro The V | Val Ala Val Pro | Tyr Leu Gly Ala | Pro |
| 115 | 1 | 120 | 125 | • |
| CTT ACG TCT GTA | CGG CAG CAT | STG GAC CTG ATG | GTG GGG GCG GCC | ACC 432 |
| | Arg Gln His ' | Val Asp Leu Met | Val Gly Ala Ala | Thr |
| 130 | 135 | | 140 | |
| TTA TGC TCT GCC | CTC TAC ATC | GGA GAC CAT TGC | GGA GGT GTC TTC | TTG 480 |
| Leu Cys Ser Ala | Leu Tyr Ile (| Gly Asp His Cys | Gly Gly Val Phe | |
| 145 | 150 | 155 | | 160 |
| GCA GGG CAG ATG | GTC AGT TTC | CAA CCC CGG CGT | CAT TGG ACT ACC | CAG 528 |
| Ala Gly Glm Met | Val Ser Phe | Gln Pro Arg Arg | His Trp Thr Thr | Gln |
| | 165 | 170 | 175 | |

(2) INFORMATION FOR SEQ ID NO: 178:

180

GCC

Ala

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: procein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

SUBSTITUTE SHEET (RULE 26)

GAT TGC AAC TGT TCC ATC TAT GTG GGC CAC ATC ACC GGC CAC AGG ATG

Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met

Thr Cys Gly Phe Ala Asp Leu M t Gly Tyr Ile Pro L u Val Gly Ala

Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

Ser Ile Phe Leu Leu Val Leu Leu Ser Arg Leu Thr Val Pro Ala Ser

Ala Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys

Trp Ile Pro Leu Thr Pro Thr Val Ala Val Pro Tyr Leu Gly Ala Pro
115 120 125

Leu Thr Ser Val Arg Gln His Val Asp Leu Met Val Gly Ala Ala Thr 130 140

Leu Cys Ser Ala Leu Tyr Ile Gly Asp His Cys Gly Gly Val Phe Leu 145 155 155 160

Ala Gly Gln Met Vai Ser Phe Gln Pro Arg Arg Mis Trp Thr Thr Gln
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met 180 185 190

Ala

- (2) INFORMATION FOR SEQ ID NO: 179:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) PEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..579

| | 179: | NO: | TD | SEO | DESCRIPTION: | SEQUENCE | (xi) |
|--|------|-----|----|-----|--------------|----------|------|
|--|------|-----|----|-----|--------------|----------|------|

| ACCTGCGGCT | TCGCCGACCT | CATGGGATAC | ATCCCGCTCG | TAGGCGCCCC | CGTGGGAGGC | 60 |
|------------|------------|------------|------------|------------|------------|-------|
| GTCGCCAGAR | CTCTGGCGCA | TGGCGTCAGG | GCTCTGGAAG | ACGGGATCAA | TTATGCAACA | 120 |
| GGGAATCTTC | CTGGTTGCTC | TITCTCTATC | TOCOTTOTTG | AACTTCTCTC | GTGCCTGACT | 180 |
| GTTCCCGCCT | CAGCCATCCA | CTATCUCAAT | GCTTCGGACG | GITATTATAT | CACCAATGAT | 240 |
| TGCCCGAACT | CTAGCATAGT | GTATGAAGCC | GAGAACCACA | TCTTGCACCT | TCCGGGGTGT | 300 |
| ATACCCTGTG | TGAAGACCGG | GAATCAGTCG | CSGTGCTGGG | TGGCTCTCAC | CCCCACGCTG | 360 |
| eceeccccyc | ACCTACGTGC | TCCGCTTTCG | TCCTTACGGG | CGCATGTGGA | CCTAATGGTG | _ 420 |
| GGGGCCGCCA | CGGCATGCTC | CGCTTTTTAC | ATTGGAGATC | TGTGCGGGG | TGTGTTTTTG | 480 |
| GCGGGCCAAC | TGTTCACTAT | CCGGCCACGC | ATTCATGAAA | CCACTCAGGA | CTGCAATTGC | 540 |
| TCCATCTACT | CAGGGCACAT | CACGGGTNNN | NNNNNNNNN | | | 579 |

(2) INFORMATION FOR SEQ ID NO: 180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1 5 10 15

Pro Val Gly Gly Val Ala Arg Xaa Leu Ala His Gly Val Arg Ala Leu 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

Ser Ile Ser Leu Leu Glu Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 60

Ala Ile His Tyr Arg Asn Ala Ser Asp Gly Tyr Tyr Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Var Tyr Glu Ala Glu Asn His Ile Leu Ris 85 90 95

Leu Pro Gly Cys Ile Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys 100 105 110



| Trp | Val | Ala 115 | Leu | Thr | Pro | Thr | Leu 120 | Ala | Ala | Bro | His | Leu 125 | Arg | Ala | Pr |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|-------------------|------------|------------|------------|------------|------------|-----|
| Leu | S r 130 | Ser | Leu | Arg | Ala | His 135 | Val | Asp | Leu | Met | Val 140 | Gly | Ala | Ala | Th |
| Ala 145 | Cys | Se: | Ala | 7he | Tyr 150 | Ile | Gly | ДSp | Leu | Cys 155 | Gly | Gly | Val | Phe | Let |
| Ala | Gly | Gln | Leu | Phe 165 | Thr | Ile | Arg | Pro | Arg 170 | Ile | His | Glu | Thr | Thr 175 | Gl: |
| Asp | Суз | Asn | Суs 180 | Ser | Ile | Tyr | Ser | Gly 185 | Zis | Ile | Thr | Gly | Xaa 190 | Xaa | Xaa |
| Xaa | | | | | | | | | | | | | | | |

- (2) INFORMATION FOR SEQ ID NO: 181:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 (B) LOCATION: 1..578
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

| GCGTGCGGCT | TCGCCGATCT | CATGGGATAC | ATCCCGCTCG | TAGGCGCCCC | CGTGGGTGGC | 60 |
|------------|------------|------------|------------|------------|------------|-----|
| GTCGCCAGAG | CCCTGGCGCA | CGGTGTTAGG | GCTGTGGAGG | ACGGGATTAA | CTACGCAACA | 120 |
| GGGAATCTTC | CTGGTTGCTC | TTTCTCTATC | TNCCTTCTGG | CACTTCTCTC | GTGCCTGACT | 180 |
| GTCCCGGCCT | CGGCTCAGCA | CTACCGGAAT | GTCTCGGGCA | TCTACCACGT | CACCAATGAT | 240 |
| TGCCCGAATT | CCAGCATAGT | GTATGAAGCC | GATCACCACA | TCATGCACTT | ACCAGGGTGC | 300 |
| ATACCCTGCG | TGAGGACCGG | GAACGTTTCG | CGCTGCTGGG | TATCTCTGAC | ACCTACTGTG | 360 |
| GCTGCTCCCT | ACCTCGGGGC | TCCGCTTACG | TCGCTACGGC | GGCATGTGGA | TTTGATGGTG | 420 |
| GGTGCAGCCA | CCCTTTGCTC | TGCCCTCTAC | GTCGGAGACC | TCTGTGGAGG | TGTCTTCCTA | 480 |



GTGGGACAGA TGTTCACCTT CCAGCCGCGC CGCCACTGGA CCACTCAGGA CTGCAACTGC 540
TCCATTTACG TCGGCCACAT CACAGGCCAC AGAATGGCT 579

(2) INFORMATION FOR SEQ ID NO: 182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (8) TYPS: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:
- Ala Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1 5 10 15
- Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30
- Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45
- Ser Ile Xaa Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60
- Ala Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp 65 70 75 80
- Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His 85 90 95
- Leu Pro Gly Cys Ile Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys
 100 105 110
- Trp Val Ser Leu Thr Pro Thr Val Ala Ala Pro Tyr Leu Gly Ala Pro 115 120 125
- Leu Thr Ser Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140
- Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 155 160
- Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175
- Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: \$79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

| ACC Thr | TGC Cys | GGC Gly | TTT | GCC Ala 5 | GAC As p | CTC Leu | ATG Met | GGA Gly | TAC Tyr 10 | ATC Ile | CCG | CTC | GTA Val | GGC Gly 15 | GCC Ala | 48 |
|------------------|------------------|------------------|-------------------|------------------|--------------------|------------------|------------------|-------------------|------------------|--------------------|------------------|------------------|-------------------|------------------|------------------|-----|
| CCT Pro | GTG Val | GGT Gly | GGC Gly 20 | GTC Val | GCC Ala | AGG Arg | GCC Ala | CTA Leu 25 | GAA Glu | CAC His | GGT Gly | GTT Val | AGG Arg 30 | GCT Ala | GTG Val | 96 |
| GAG Glu | GAC Asp | GGT Gly 35 | ATT Ile | AAT Asn | TAT Tyr | GCA Ala | ACA Thr 40 | GGG Gly | AAT Asn | CTC Leu | CCC | GGT Gly 45 | TGC Cys | TCT Ser | TTT Phe | 144 |
| TCT | ATC Ile 50 | TCC Ser | CTC Leu | TTG Leu | GCA .Ala | CTT Leu 55 | CTT Leu | TCG Ser | TGC Cys | CTG Leu | ACT Thr 60 | GTT Val | Pro CCC | ACC Thr | TCA Ser | 192 |
| GCC Ala 65 | GTC Val | AAC Asn | TAT Tyr | CGC Arg | AAC Asn 70 | GCC Ala | TCG Ser | GGC Gly | GTC Val | TAT Tyr 75 | CAT His | ATC Ile | ACC Thr | AAT Asn | GAC Asp 80 | 240 |
| TGC Cys | CCG Pro | AAT Asn | TCG Ser | AGC Ser 85 | ATA Ile | GTG Val | TAC Tyr | GAG Glu | GCT Ala 90 | GAC A sp | TAC Tyr | CAC His | ATC Ile | CTA Leu 95 | CAC His | 288 |
| CTC Leu | CCT Pro | GGG Gly | TGC Cys 100 | TTA Leu | CCC Pro | TGC Cys | GTG Val | AGG Arg 105 | GTT Val | GGG G1y | AAT Asn | CAG Gln | TCA Ser 110 | CGC Arg | TGC Cys | 336 |
| TGG Trp | GTG Val | GCC Ala | CTT Leu | ACT Thr | CCC Pro | ACC Thr | GTG Val | GCG Ala | GCG Ala | CCT Pro | TAC Tyr | GTT Val | GGT Gly | GCT Ala | CCG Pro | 384 |

Ala

| | 115 | | | 120 | | | 125 | | | |
|------------|-----|--|-------------------|-----|--|---|-----|--|---|-----|
| | | | AGT Ser | | | | | | | 432 |
| | | | TAC Tyr 150 | | | | | | | 480 |
| | | | TCT Ser | | | | | | | 528 |
| GAC Qea | | | ATC Ile | | | | | | | 576 |
| GCA | | | | | | • | | | - | 579 |

- (2) INFORMATION FOR SEQ ID NC: 184:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser 50 55 60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys
100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro 115 120 125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140

Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175

AST Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met

Ala

- (2) INFORMATION FOR SEQ ID NO: 182:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Ala Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Ser Phe Trp His Phe Ser Arg Ala • Leu Ser Arg Pro Arg
50 55 60

Leu Ser Thr Thr Gly Met Ser Arg Ala Ser Thr Thr Ser Pro Met Ile
65 70 75 80

Ala Arg Ile Pro Ala . Cys Met Lys Pro Ile Thr Thr Ser Cys Thr 85 90 95

Tyr Gln Gly Ala Tyr Pro Ala • Gly Pro Gly Thr Phe Arg Ala Ala 100 105 110

Gly Tyr Leu • His Leu Leu Trp Leu Leu Pro Thr Ser Gly Leu Arg

Leu Arg Arg Tyr Gly Gly Met Trp Ile * Trp Trp Val Gln Pro Pro 130 140

Phe Ala Leu Pro Ser Thr Ser Glu Thr Ser Val Glu Val Ser Ser • 145 150 155

Trp Asp Arg Cys Ser Pro Ser Ser Arg Ala Ala Thr Gly Pro Leu Arg

Thr Ala Thr Ala Pro Phe Thr Ser Ala Thr Ser Gln Ala Thr Glu Trp

180

190

| 121 | INFORMATION | ECB | 850 | TD | NO . | 185. |
|-----|-------------|-------|-----|----|------|------|
| 121 | IMPURMALLUM | 5 V N | 350 | | AU: | 703: |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 579 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..579

(ix) FEATURE:

(A) NAME/KEY: mat peptide

(B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 5 10 15

CCC GTG GGT GGC GTC GCC AGA GCC CTG GAA CAT GGT GTT AGG GCT GTG

Pro Val Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val

20

25

30

GAG GAC GGC ATC AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTC

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

40

45

TCT ATC TAC CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser

GCC ATC CAC TAT CGC AAT GCC TCG GGC GTC TAC CAC GTC ACC AAT GAC
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
70
75
80

TGC CCG AAC TCG AGC ATA GTG TAC GAG GCC GAC CAC CAC ATC CTA CAC

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His

CTT CCA GGG TGC TTA CCC TGT GTG AGG GTT GGG AAT CAG TCA CGT TGT
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys
100 105 110

TGG GTG GCC CTC TCT CCC ACC GTG GCG GCG CCT TAC ATC GGT GCT CCA 384

| Trp | Val | Ala 115 | Leu | Ser | Pro | Thr | Val 120 | Ala | Ala | Pro | Tyr | Ile 125 | | Ala | Pro | |
|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|------------|
| GTT Val | GAA Glu 130 | TCC | TTC Phe | CGG Arg | AGA Arg | CAC His 135 | GTG Val | gac Asp | ATG Met | ATG Met | GTG Val 140 | Gly | GCT Ala | GCT Ala | ACT Thr | 432 |
| GTG Val 145 | cys | TCC Ser | GCT Ala | CTC Leu | TAT Tyr 150 | ATT Ile | GGG Gly | GAC Asp | TTG Leu | TGT Cys 155 | GGT Gly | GGC Gly | GTA Val | TTC | TTG Leu 160 | 480 |
| GTT Val | ggt Gly | CAG Gln | ATG Mec | TTT Phe 165 | TCT Ser | TTC Phe | CGG Arg | CCA Pro | CGA Arg 170 | CGC Arg | EYC | TGG Trp | ACT Thr | ACG Thr 175 | CAG Gln | 528 |
| GAC Asp | TGC Cys | AAT Asn | TGT Cys 180 | TCC Ser | ATC Ile | TAC Tyr | GCG Ala | GGG Gly 185 | CAC His | ATC Ile | ACT Thr | GGC Gly | CAC Bis 190 | GGA Gly | ATG Met | 576 |
| GCA Ala | | | | | | | | | | | | | | | | 579 |

- (2) INFORMATION FOR SEQ ID NO: 186:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser 50 55 60

Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His 85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asa Glm Ser Arg Cys

Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro 115 120 125

| 23/ | |
|--|-----|
| Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr 130 135 140 | |
| Val Cys S r Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 155 160 | |
| Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln 165 170 175 | |
| Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met 180 185 190 | |
| Ala | |
| (2) INFORMATION FOR SEQ ID NO: 187: | |
| (i) SEQUENCE CHARACTERISTICS: | |
| (A) LENGTH: 579 base pairs | |
| (B) TYPE: nucleic acid (C) STRANDEDNESS: single | |
| (D) TOPOLOGY: linear | |
| (ii) MOLECULE TYPE: cDNA | |
| (iii) HYPOTHETICAL: NO | |
| (iii) ANTI-SENSE: NO | |
| (ix) FEATURE: | |
| (A) NAME/KEY: CDS | |
| (B) LOCATION: 1579 | |
| (ix) FEATURE: | |
| (A) NAME/KEY: mat_peptide | |
| (B) LOCATION: 1576 | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187: | |
| ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC | 48 |
| Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala | |
| 1 5 10 15 | |
| CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG | 96 |
| Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30 | |
| | |
| GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CIT CCC GGT TGC TCT TTC Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe | 144 |
| 35 40 45 | |
| TCT ATC TTC CTC TTG GCA CTT CTT-TCG TGC CTG ACT GTT CCC ACC TCG | 107 |
| Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser | 192 |
| 50 55 60 | |

SUBSTITUTE SHEET (RULE 26)

GCC GTC AAC TAT CGC AAT GCC TCG GGC ATC TAT CAC ATC ACC AAT GAC



| | Ala 65 | Val | Ast | Tyr | Arg | Asn 70 | Ala | Ser | Gly | 11 | Tyr 75 | His | Ile | Thr | Asn | Asp 80 | |
|---|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| | TGC | Pro | AAC | TCG Ser | AGC Ser 85 | ATA Ile | GTG Val | TAC Tyr | GAG Glu | ACC Thr 90 | GAG Glu | CAC His | CAC His | ATC Il | CTA Leu 95 | CAC His | 288 |
| | CTC | Pro | GGG Gly | TOO TGT | TTA Leu | 520 CCC | Cya Cya | GTS Val | AGG Arg 105 | GII Val | GGG Gly | AAT Asn | CAG Gla | TCA Ser 110 | % ೧೮೮ | TGC Cys | 336 |
| | TGG Trp | GTG Val | GCC Ala 115 | CTC Leu | ACT Thr | DIO CCC | ACC Thr | GTG Val 120 | GC3 Ala | GCG Ala | CCT Pro | TAC Tyr | ATC Ile 125 | GGC Gly | GCT Ala | CCG Pro | 384 |
| | CTT Leu | GAA Glu 130 | TCC Ser | CTC Leu | CGG Arg | AGT Ser | CAT His 135 | GTG Val | GAT A sp | CTG Leu | ATG Mec | GTA Val 140 | GGT Gly | GCC Ala | GCT Ala | ACT Thr | 432 |
| | GCG Ala 145 | TGC Cys | TCC Ser | GCT Ala | CTT Leu | TAC Tyr 150 | ATC Ile | GGA Gly | GAC Asp | CTG Leu | TGC Cys 155 | GGT Gly | GGC Gly | GTA Val | TTT Phe | TTG Leu 160 | 480 |
| 1 | GTT Val | GGT Gly | CAG Gln | Met | TTC Phe 165 | TCT Ser | TTC Phe | CAG Gl:: | Pro CCG | CGG Arg 170 | YZ3 CGC | CAC His | TGG Tep | The | ACG Thr 175 | CAG Gln · | 529 |
| 1 | GAC Asp | TGC Cys | AAT Asn | TGT Cys 180 | TCC Ser | ATC Ile | TAC Tyr | Ala | GGG Gly 185 | CAC His | GIT Val | ACG Thr | GGC Gly | CAC His 190 | AGG Arg | ATG Met | 576 |
| | SCA Ala | | | | | | | | | | | | | | | | 579 |

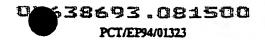
- (2) INFORMATION FOR SEQ ID NO: 188:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val

Glu Asp Gly Ile Asn Tyr Ala Thr-Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser 50 55 60



Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Il Val Tyr Glu Thr Glu His His Ile Leu His 85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys

Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro 115 120 125

Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140

Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 155 160

Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 189:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...579
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 5 10 15

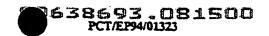
48



| ccc | . كبا | . ccc | ccc | GTC | cca | 3.00 | | ~~~ | | | • | | | | | | |
|------|-------|----------|----------------|-----|------------|------|-----------------|-----|-----|------------|-------|-------------|--------------|--------------|------|-----------|--|
| Pro | Val | Glv | Glv | Val | Ala | Ara | Ala | CTG | 31. | CAT | GGC | GTC | AGG | CCI | GTG | 96 | |
| | | | 20 | | | 3 | ~~ | 25 | ~~ | 4-5 | GTÀ | val | A29 | Ala | Val | | |
| | | | | | | | | | | | | | | | | | |
| GYC | GAC | GGG | ATT | AAC | TAT | GCG | ACA | GGG | AAT | CII | CCC | GGT | TGC | TCT | TTC | 144 | |
| GIU | Asp | GIÀ | Ile | Asn | Tyr | Ala | Thr | Gly | YZD | Leu | PTO | Gly | Cys | Ser | Phe | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| TCT | ATC | TTC | CTC | CIG | GCX | CTT | CIT | TCG | TGC | | 3~ | GTC | ~~ | ccc | 703 | 1.00 | |
| Ser | Ile | Phe | Leu | Leu | Ala | Leu | Leu | Ser | Cys | Leu | The | Val | Pro | Ala | Ser | 192 | |
| | 50 | | | | | 55 | | | • | | 60 | | | | ••• | | |
| نسان | CSC | a | m> 0 | ~~~ | | | | | | | | | | | | | |
| Ala | GAG | Wie | TAC | N | AAT | GCT | TCG | GGC | ATC | TAT | CXC | ATC | ACC | AAT | GAC | 240 | |
| 65 | | 413 | 171 | ~~3 | Asa 70 | MIG | 261 | GTÅ | -16 | 75 | His | Ile | Thr | Asn | | | |
| | | | | | | | | | | /3 | | | | | 80 | | |
| TGT | CCG | AAT | TCC | AGC | GTA | GTC | TAT | GAA | ACT | GAC | CAC | CAT | ATA | TTG | CAC | 288 | |
| Cys | Pro | Asn | Ser | Ser | Val | Val | Tyr | Glu | Thr | qz, | His | His | Ile | Leu | His | • | |
| | | | | 85 | | | | | 90 | | | | | 95 | | • | |
| TIG | CCG | GGG | TGC | GTA | CCC | TCC | GTG | 302 | ~~~ | | | | | | | | |
| Leu | Pro | Glv | Cvs | Val | Pro | Cvs | Val | 7~~ | 314 | GLV | 300 | G.G | TCT | CGT | TGC | 336 | |
| | | • | 100 | | | -,- | | 105 | | 9.7 | A3.: | Vd. | 110 | Arg | Cys | | |
| | | | | | | | | | | | | | | | | | |
| TGG | ACG | CCG | GTA | ACA | CCT | ACG | GTG | CCT | CCC | GTA | TCC | ATG | GAC | GCT | CCG | . 384 | |
| ım | Thr | Pro | Val | The | Pro | Thr | | λia | λla | Va: | Ser | Met | Asp | Ala | Pro | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| CIC | GAG | TCC | TTC | CGG | CGG | CAT | GTG | GAC | СТА | 276 | GT2 | COT | ccc | ecc | NCC | 432 | |
| Leu | Glu | Ser | Phe | Arg | Arg | Ris | Val | ASD | Leu | Met | Val | G1 v | Ala | Ala | Thr | 432 | |
| | 130 | | | | | 135 | | • | | | 140 | | | | | | |
| | | | | | | | | | | | | | | | | | |
| Ual | TGT | TCT | GTC | CTC | TAT | GIT | GGA | GAC | CIC | TGT | GGA | GGT | GCT | TTC | CTA | 480 | |
| 145 | Cys | 361 | vaı | rea | Ty: 150 | val | GIĀ | ASP | ren | Cys 155 | Gly | Gly | Ala | Phe | | | |
| | | | | | | | | | | 733 | | | | | 160 | | |
| GTG | GGG | CAG | ATG | TTC | ACC | TTC | CAG | CCG | CGT | CGC | CAC | TGG | ACC | ACG | CAG | 528 | |
| Val | Gly | Gln | Met | Phe | Thr | Phe | Gln | Pro | Arg | Yzā | Eis | ŢŢ | Thr | Thr | Gln | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | |
| GAT | TGT | ΔΔΤ | ፐርረ | TCC | ATC | тэт | ب ے2 | cee | C>= | 3 | | 000 | a > - | | | . | |
| Asp | Cys | Asn | Cvs | Ser | Ile | Tvr | Th= | Glv | His | Tie | みじご | GGC | CAC | AGG | ATG | 576 | |
| • | • - | | 180 | | | -,- | | 185 | | ••• | * *** | 3- 3 | 190 | ~ _'y | ne C | | |
| | | | | | | | | | | | | | | | | | |
| GCG | | | | | | | | | | | | | • | | | 579 | |
| Ala | | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: procein



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asm Tyr Ala Thr Gly Asm Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55 60

Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys
100 105 110

Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro

Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr 130 135 140

Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu 145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met 180 185 190

Ala

- (2) INFORMATION FOR SEQ ID NO: 191:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS



(B) LOCATION: 1..289

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..286

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

| ATG Met 1 | AGC Ser | ACG | AAT Asn | CCT Pro 5 | aaa Lys | CCT | CAA Gln | AGA Arg | AAA Lys 10 | ACE Thr | AAA Lys | CGT | AAC Asti | ACC Thr 15 | AAC Asn | | 48 |
|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|---|-------|
| CGC Arg | CGC | Pro CCC | ATG Met 20 | gac Asp | GTT Val | AAG Lys | TTC Phe | CCG Pro 25 | G] Y GGC | GGT Gly | GGC Gly | CAG Gln | ATC Ile 30 | GTT Val | GGT Gly | | 96 |
| GGA Gly | GTT Val | TAC Tyr 35 | TTG Leu | TTG Leu | 510 CC3 | Yza CCC | AGG Arg 40 | GGC | Pro | λGG λrg | TTG Leu | GGT Gly 45 | GTG Val | yrg | GCG Ala | | - 144 |
| ACT Thr | AGG Arg 50 | AAG Lys | ACT Thr | TCG Ser | GAG Glu | CGG Arg 55 | TCG Ser | CAA Gln | Pro | CGT Arg | GGG Gly 60 | AGA Arg | CGT Arg | CAG Gln | 510 CCI | | 192 |
| ATC Ile 65 | CCC Pro | AAG Lys | GCA Ala | CGT Arg | CGA Arg 70 | TCT Ser | GAG Glu | GGA Gly | AGG Arg | TCC Ser 75 | TGG Trp | GCT Ala | CAG Gln | CCC | GGG Gly 80 | | 240 |
| TAC Tyr | CCA Pro | TGG Trp | CCT Pro | CTT Leu 85 | TAC Tyr | GGT Gly | AAT Asn | GAG Glu | GGT Gly 90 | TGT Cys | GGG Gly | TGG Trp | GCA Ala | GGA Gly 95 | TGG Trp | G | 289 |

(2) INFORMATION FOR SEQ ID NO: 192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60

Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly

65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp 85 90 95

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..498

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

| ATG | AGC | ACG | AAT | CCT | AAA | CCT | CAA | AGA | AAA | ACC | KKA | CGT | AAC | ACC | AAC | 48 |
|-----|-----|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Thr | Asn | Pro | Lys | Pro | Gln | Azg | Lys | The | Lys | Arg | Asn | Thr | Asn | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| | | | | | | | | | | | | | | | | |
| | | | | | GTA | | | | | | | | | | | 96 |
| Arg | Arg | Pro | Met | Asp | Val | Lys | Phe | Pro | Gly | GJĀ | Gly | Gln | Ile | Val | Gly | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | - | - | | GCG | 144 |
| Gly | Val | • | Leu | Leu | Pro | Arg | - | Gly | Pro | Arg | Leu | - | Val | Arg | Ala | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| | | | | | | | | | | | | | | | | |
| | | | | | GAG | | | | | | | | | | | 192 |
| Thr | - | Lys | Thr | Ser | Glu | | Ser | GIN | Pro | ATG | | Arg | Arg | Gin | PTO | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| ልጥሮ | ccc | n n G | ece | CGC | CGG | TCC | GAG | ccc | 166 | TCC | TCC | ccc | CAA | GCC | GGG | 240 |
| | | | | | Arg | | | | | | | | | | | |
| 65 | 210 | Lys | Ala | 4-3 | 70 | 361 | 914 | 923 | ~~3 | 75 | TTP | ~ | 91 | ~-4 | 80 | |
| 0.5 | | | | | , , | | | | | | | | | | - | |
| TAC | ccc | TGG | ccc | стс | TAT | GGC | AAT | GAG | GGC | TGT | GGG | TGG | GCA | GGG | TGG | 288 |
| | | | | | Tyr | | | | | | | | | | | |
| • | | • | | 85 | • | • | | | 90 | • | • | • | | 95 | _ | |
| | | | | | | | | | | | | | | | | |
| CTC | CTG | TCT | CCT | CGC | GGC | TCT | CGG | CCA | TCT | TGG | GGC | CCA | AAT | GAT | CCC | 336 |



| Leu | Leu | Ser | Pro 100 | Arg | Gly | Ser | Arg | Pro 105 | Ser | £ | Gly | Pro | Asn 110 | Asp | Pro | |
|-------------------|------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|------------|-------------------|-------------------|-------------------|------------|------------|-------------------|-----|
| CGG | CGG Arg | AGA Arg 115 | TCG Ser | CGC Arg | aat Asn | CTG Leu | GGT Gly 120 | AAG Lys | GTC Val | ATC Ile | GAT Asp | ACC Thr 125 | CTG Leu | ACG Thr | TGC Cya | 384 |
| GGC Gly | Phe 130 | GCC Ala | GAC Asp | CTC Leu | ATG Met | GGA Gly 135 | TAC Tyr | ATC Ile | CCG | CTC | GTG Val 140 | GGC Gly | GCC Ala | CCC Pro | GTC Val | 432 |
| GGG Gly 145 | GIY | GTC Val | GCC Ala | AGG Arg | GCC Ala 150 | CTG Leu | GCG Ala | CAT His | Gly | GTC Val 155 | AGG Arg | GCT Ala | GTG Val | GAG Glu | GAC Asp 160 | 480 |
| GGG Gly | | | | CGA Arg 165 | | | | | | | | | | | | 498 |

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1 5 10 15

Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala
35 40

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro 50 55 60

Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Ala Gly 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro 100 105 110

Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys 115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val 130 140



| VO 94/25601 | | 638693 . (PCT/EP94/0 |
|-------------|---|---------------------------|
| | 245 | _ |
| Gly Gly | Val Ala Arg Ala Leu Ala His Gly Val Ar 150 155 | rg Ala Val Glu Asp 160 |
| Gly Ile | Asn Tyr Arg Gln 165 | |
| (2) INFO | PRMATION FOR SEQ ID NO: 195: | |
| (i) | SEQUENCE CHARACTERISTICS: (A) LENGTH: 579 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (ii) | MOLECULE TYPE: cDNA | |
| (111) | HYPOTHETICAL: NO | - |
| (iii) | ANTI-SENSE: NO | |
| (ix) | FEATURE: | |
| | (A) NAME/KEY: CDS . (B) LOCATION: 1579 | |
| (ix) | FEATURE: | |
| | (A) NAME/KEY: mac_peptide | |
| | (B) TOCKETON 1 PEC | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

| ACG | TGC | GGA | TTC | GCC | GAC | CIC | GTG | GGG | TAC | ATC | CCG | CIC | GTA | GGC | GGC | 48 |
|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|
| Thi | Cys | GIY | Phe | _ | Asp | Leu | Val | Gly | | Ile | Pro | Leu | Val | Gly | Gly | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| CCC | GTT | GGG | GGC | GTC | GCX | AGG | GCT | CTC | GCA | CYI | GGT | GTG | AGG | GTT | CII | 96 |
| Pro | Val | Gly | | Val | Ala | Arg | Ala | Leu | Ala | His | Gly | Val | Arg | Val | Leu | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| GAG | GAC | GGG | GTG | AAT | TAT | GCA | ACA | GGG | AAT | CTG | CCT | GGT | TGC | TCT | TTC | 144 |
| Glu | Asp | Gly | Val | Asn | Tyr | Ala | Thr | Gly | Asn | Leu | Pro | Gly | Cys | Ser | Phe | |
| | | 35 | | | | | 40 | | | | | 45 | · | | | |
| | | | | | | | | | | | | | | GCC | | 192 |
| Ser | Ile | Phe | Ile | Leu | Ala | Leu | Leu | Ser | Cys | Leu | Thr | Val | Pro | Ala | Ser | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| | | | | | | | | | | | | | | AAT | | 240 |
| Ala | Val | Pro | Tyr | Arg | Asa | Ala | Ser | Gly | Ile | Tyr | His | Val | Thr | Asa | Asp | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| TGC | CCA | AAC | TCT | TCC | ATA | GTC | TAT | ·GAG | GCA | GAT | GAT | CTG | ATC | CTA | CAC | 288 |
| Cys | Pro | Asn | Ser | Ser | Ile | Val | Tyr | Glu | Ala | Asp | Asp | Leu | Ile | Leu | His | |
| | | • | | 85 | | | | | 90 | , | • | | | 95 | | |
| GCA | CCT | GGC | TGC | GTG | CCT | TGT | GTC | AGG | AAA | GAT | AAT | GTG | AGT | AGG | TGC | 336 |



| Ala | Pro | Gly | Cys 100 | Val | Pro | Cys | Val | Arg 105 | Lys | Asp | Asn | Val | Ser 110 | Arg | Cys | | |
|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|---|-----|
| TGG Trp | GTC Val | CAA Gln 115 | ATT Ile | ACC Thr | Pro | ACG Thr | CTG Leu 120 | TCA Ser | GCC | CCG | AGC Ser | TTC Phe 125 | GGA Gly | GCA Ala | GTC Val | | 384 |
| ACG Thr | GCT Ala 130 | Pro | CTT Leu | Yrg CGG | AGA Arg | GCC Ala 135 | GIT Val | GAT Asp | TAC Tyr | TTG Leu | GTG Val 140 | GGA Gly | GGG Gly | GCT Ala | GCC Ala | | 432 |
| CTC Leu 145 | TGC Cys | TCC Ser | GCG Ala | TTA Leu | TAC Tyr 150 | GTT Val | GGA Gly | GAC Asp | GCG Ala | TGT Cys 155 | GGG Gly | GCA Ala | CTA Leu | TTT Phe | TTG Leu 160 | | 480 |
| Val | Gly | Gln | Mec | Phe 165 | ACC Thr | Tyr | Arg | Pro | Arg 170 | Gln | His | Ala | Thr | Val 175 | Gln | • | 529 |
| Asp | CYS | AAC Asn | TGT Cys 180 | TCC Ser | ATC Ile | TAC Tyr | AGT Ser | GGC Gly 185 | CAC His | GTC Val | ACC Thr | GGC Gly | CAT His 190 | CAG Gln | ATG Met | | 576 |
| GCA Ala | | | | | | | | | | | | | | | | ! | 579 |

- (2) INFORMATION FOR SEQ ID NO: 196:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly
1 5 10 15

Pro Val Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu 20 25 30

Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe 35 40 45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser 50 55

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His 85 90 95

Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys 100 105 110



Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu 145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..579
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..576
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

| ACT | TGC | GGC | TIT | GCC | GAC | CTC | ATG | GGA | TAC | ATC | CCG | CIC | GTA | GGC | GCC | 48 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Thr | Cvs | Gly | Phe | Ala | Asp | Leu | Met | Gly | Tyr | Ile | Pro | Leu | Val | Gly | Ala | |
| 1 | • | • | | 5 | - | | | | 10 | | | | | 15 | | |

CCC GTG GGT GGC GTC GCC AGA GCC CTG GAA CAT GGT GTT AGG GCT GTG

Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val

20 25 30

GAG GAC GGC ATC AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTC 144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe
35 40 45

TOT ATO THE CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG 192



| Se | r Ile 50 | Ty 2 | r Leu | Leu | Ala | Leu SS | Leu | Sez | Cys | Leu | Thr 60 | | Pro | Thr | Ser | |
|-------------------|-------------------|-------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|------|
| 6 | 5 | | | Mrg | 70 | ALA | ser | erA | ' Val | Ty: 75 | His | Val | Thr | Asn | GAC Asp 80 | 240 |
| -7- | | | . 361 | 85 | ATA Ile | AGT | IYE | Glu | 90 | Asp | His | His | Ile | Leu 95 | His | 288 |
| | | OL, | 100 | Dea | CCC Pro | Cys | vaı | 105 | Val | Gly | Asn | Gln | Ser 110 | Arg | Суз | 336 |
| | | 115 | ueu | Jes | Pro CCC | inr | 120 | Ala | Ala | Pro | Tyr | Ile 125 | Gly | Ala | Pro | 384 |
| GTT Val | GAA Glu 130 | TCC Ser | TTC Phe | Arg | AGA Arg | CAC His 135 | GTG Val | GAC Asp | ATG Met | ATG Met | GTG Val 140 | GGC Gly | GCT Ala | GCT Ala | ACT Thr | 432 |
| GTG Val 145 | TGC Cys | TCC Ser | GCT Ala | ren | TAT Tyr 150 | ATT Ile | GGG Gly | GAC Asp | TTG Leu | TGT Cys 155 | GGT Gly | GGC Gly | GTA Val | TTC Phe | TTG Leu 160 | 480 |
| GTT Val | GGT Gly | CAG Gln | wec | TTT Phe 165 | TCT : | TTC Phe | CGG Arg | CCA Pro | CGA Arg 170 | CGC | CAC His | TGG Trp | ACT Thr | ACG Thr 175 | CAG Gln | 5.28 |
| ra p | TGC Cys | MSII | TGT Cys 180 | TCC . Ser | ATC : Ile : | rac (Tyr) | Ala | GGG Gly 185 | CAC His | ATC Ile | ACT Thr | GGC | CAC His 190 | GGA Gly | ATG Mec | 576 |
| GCA Ala | | | | | | | | | | | | | | | | 579 |

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala

1 5 10 15

Pro Val Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

35

40

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser 50 55

Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His
85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys

Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro 115 120 125

Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr 130 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu 145 150 155 160

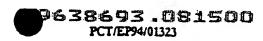
Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1470 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..1470
- (ix) FEATURE:
 - (A) NAME/KEY: mat peptide
 - (B) LOCATION: 2..1467
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:



| | 1 | ••• | 7.0 | GAG Glu | 5 | Leu | ser : | H1S ' | Thr | 10 | Leu | Thr . | Ala | Sez | Ser 15 | 46 |
|-------------------|-------------------|-------------------|-----------------------|-----------------------|-------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------|
| | | . u. 146 | | 2 | 0 | r GTI | I AL | a Ali | 2 Arg | g Me | t Th | • | Se | 7 TY | | |
| AC Th | G AG | T GC | | TT CC ie Pr is | C AG | G ACC | Pro | A CCI Pro 40 |) Pro | A TTO Pho | TTO | G GGJ L Gly | A TA | X 1: | A CTG A Leu | 142 |
| TC Se | C TT r Le | | C AG F Ar O | g CA | G AG | A CGG | CTC Lev | 1 GIV | CTA Leu | GG(| TCC Sea | TCC Sez 60 | Se | TG(| CCA Pro | 190 |
| CG: Ar | G CC G Pr 6 | 9 21 | C CT O Le | u Pro | G GCI o Ala | GTG Val 70 | • | Gln | CGC Arg | CCC Pro | 75 | Pro | ACJ Thi | TCC Se: | AGG Arg | 238 |
| AAC Lys | ••• | p Pro | c TG o Cy | C CTO S Lev | AGG Arg 85 | Wid | GGG Gly | AGG Arg | TTC Phe | Sto CCI | Sez | ACG Thr | GC2 | GAG Glu | CCA Pro 95 | 286 |
| Phe | Pro | TTO Let | G CT | T TTX u Leu 100 | • • | AGG Arg | GTG Val | GTA Val | GGC Gly 105 | ATC Ile | TCA Ser | TCT Ser | TCT | GCC Ala 110 | | . 334 |
| Pro | AGA Arg | Lys | A AAC B Ass 11: | r GTC n Val | ATG Mec | AAC Asn | TCG Ser | CCA Pro 120 | Ser | AAC Asn | TGA • | CCA Pro | GCC Ala 125 | ΞŢ | GCG Ala | 382 |
| TGA | ACG Thr | PT0 | , 1-5 | G CAT | ATT | ATA Ile | GAG Glu 135 | GTC Val | TAG • | ACG The | TCG Ser | CCG Pro 140 | TCA Ser | TAC | CCA Pro | 430 |
| CAA Gln | CAG Gla 145 | 920 | ACC The | Trp | TCG Ser | TGT Cys 150 | GCA Ala | GCX Ala | CCG | ACG Thr | CGC Arg 155 | TCA Ser | TGA • | CGG Arg | GAT ÇaA | 478 |
| TCA Ser 160 | CCG Pro | GCG Ala | ACT | TTG Leu | ATT Ile 165 | CTG Leu | TCA Ser | TAG * | ACT Thr | GCA Ala 170 | ACT Thr | CCG Pro | CCG Pro | TCA Ser | CTC Leu 175 | 526 |
| AGA Arg | CGG Arg | TGG | ACT | TCA Ser 180 | GTC Val | TGG Trp | ATC Ile | CCA Pro | CTT Leu 185 | TTA Leu | CCA Pro | TTG Leu | AGA | CTA Leu 190 | CCA Pro | 574 |
| CAG Gln | TGC Cys | CCC | AGG Arg 195 | ACG | CAG Gln | TGT Cys | CCA Pro | GAA Glu 200 | GCC Ala | AGC Ser | GTT Val | GGG Gly | GCC Ala 205 | GCA Ala | CGG Arg | . 622 |
| GGA Gly | GAG Glu | GTA Val 210 | GLY | ACG Thr | GCA Ala | TAT Tyr | ACC Thr 215 | GGT Gly | ATG Met | TCT Ser | CGG | CTG Leu 220 | GAG Glu | AGA Arg | GAC Asp | 670 |
| CGT Arg | CTG Leu | GCA Ala | TGT Cys | TCG Ser | ACT Thr | PT0 CCG | Tzp TGG | TGC Cys | TCT | GTG Val | AGT Ser | GCT Ala | ACG Thr | ATG Me: | CCG Pro | 718 |



| | 225 | | | | | 230 | | | | | 235 | | | | | |
|-------------------|------------|------------|-------------------|------------|--------------------|------------|------------|-------------------|------------|-------------------|------------|------------|-------------------|------------|-------------------|------|
| GAT Asp 240 | GTG Val | CAT His | GGT Gly | ACG Thr | ATC Ile 245 | TGA | CTC Leu | CTG Leu | CCG Pro | AGA Arg 250 | CTA Leu | Pro CCG | TGA • | GGT Gly | TGC Cys 255 | 766 |
| | | | | | S.c.c | | | | | | | | | | | 814 |
| ATT Ile | CTG Leu | GGA Gly | GGG Gly 275 | GGT Gly | GTT Val | CAC His | GGG Gly | GCT Ala 280 | CAC His | TAA | CAT His | CGA Arg | CGC Arg 285 | TCA Ser | CAT | 862 |
| | | | | | ACA Thr | | | | | | | | | | | 910 |
| | | | | | CTG Leu | | | | | | | | | | | 958 |
| | | | | | ATG Met 325 | | | | | | | | | | | 1006 |
| | | | | | TAC Tyr | | | | | | | | | | | 1054 |
| | | | | | ACC Thr | | | | | | | | | | | 1102 |
| | | | | | AGC Ser | | | | | | | | | | | 1150 |
| | | | | | TGC Cys | | | | | | | | | | | 1198 |
| | | | | | GGG Gly 405 | | | | | | | | | | | 1246 |
| | | | | | gat A sp | | | | | | | | | | | 1294 |
| | | | | | CGT Arg | | | | | | | | | | | 1347 |
| | | | | | ACG Thr | | | | | | | | | | | 1390 |

| GCA Ala | GCC Ala 465 | ACG Thr | TCT | GTG Val | TGG | AAC Asn 470 | AAG Lys | GCT Ala | GAG Glu | CAG Gla | TTC Phe 475 | TGG Trp | CCY Bro | CAT His | ACA Thr | 1438 |
|-------------------|-------------------|------------|------------|------------|-------------------|-------------------|------------|------------|------------|------------|-------------------|------------|------------|------------|------------|------|
| TGT Cys 480 | GGÀ Gly | ACT Thr | TCA Ser | TCA Ser | GTG Val 485 | gga Gly | TAC Tyr | AAT Asn | AAT Asn | AG | | | | | | 1470 |

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

| TGTGCCAGGA | CCATCACCAC | CGGAGCTTCT | ATCACATACT | CCACTTACGG | CAAGTTCCTT | 60 |
|------------|------------|------------|------------|------------|------------|-------|
| GCTGATGGAG | GGTGTTCAGG | CGGCGCGCAT | GACGTGATCA | TATGCGACGA | GTGCCATTCC | 120 |
| CAGGACGCCA | CCACCATTCT | TGGGATAGGC | ACTGTCCTTG | ACCAGGCAGA | GACGGCTGGA | 180 |
| GCTAGGCTCG | TCGTCTTGGC | CACGGCCACC | CCTCCCGGCA | GTGTGACAAC | GCCCCACCCC | 240 |
| AACATCGAGG | AAGTGGCCCT | GCCTCAGGAG | GGGGAGGTTC | CCTTCTACGG | CAGAGCCATT | 300 |
| cccciiecii | TTATAAAGGG | TGGTAGGCAT | CTCATCTTCT | GCCATTCCAA | GAAAAAATGT | 360 |
| GATGAACTCG | CCAAGCAACT | GACCAGCCTG | GGCGTGAACG | CCGTGGCATA | TTATAGAGGT | 420 |
| CTAGACGTCG | CCGTCATACC | CACAACAGGA | GACGTGGTCG | TGTGCAGCAC | CGACGCGCTC | 480 |
| ATGACGGGAT | TCACCGGCGA | CTTTGATTCT | GTCATAGACT | GCAACTCCGC | CGTCACTCAG | 540 |
| ACGGTGGACT | TCAGTCTGGA | TCCCACTTTT | ACCATTGAGA | CTACCACAGT | GCCCCAGGAC | 600 |
| GCAGTGTCCA | GAAGCCAGCG | TTGGGGCCGC | ACGGGGAGAG | GTAGGCACGG | CATATACCGG | 660 |
| TATGTCTCGG | CTGGAGAGAG | ACCGTCTGGC | ATGTTCGACT | CCGTGGTGCT | CTGTGAGTGC | 720 |
| TACGATGCCG | GATGTGCATG | GTACGATCTG | ACTCCTGCCG | AGACTACCGT | GAGGTTGCGC | 780 |
| GCTTACNTAA | ACACCCCCGG | GCTCCCTGTC | TGTCAGGACC | ATTTGGAATT | CTGGGAGGGG | . 840 |
| GTGTTCACGG | GGCTCACTAA | CATCGACGCT | CACATGCTGT | CACAGACCAA | ACAGGGTGGG | 900 |
| GAGAATTTCC | CATACCTTGT | AGCGTACCAA | GCAACAGTCT | GTGTTCGCGC | GAAAGCGCCC | 960 |



| CCCCCCAGCT | GGGACACAAT | GTGGAAATGC | ATGCTCCGTC | TCAAACCGAC | NTTAACTGGC | 1020 |
|------------|------------|------------|------------|------------|------------|------|
| CCTACTCCCC | TCTTGTACAG | GCTGGGGCCC | GTCCAGAATG | AGATCACACT | GACGCACCCC | 1080 |
| ATCACCAAGT | ACATTATGGC | TTGCATGTCT | GCGGACTTGG | AGGTCATTAC | CAGCACTTGG | 1140 |
| GTTCTGGTGG | GGGGGTTGT | GGCGGCCCTG | GCGGCCTACT | GCTTGACGGT | GGGTTCGGTA | 1200 |
| | GTAGGATCAT | | | | | 1260 |
| TTATACCAGC | AATTTGATGA | GATGGAGGAG | TECTCEGCCT | CGTTGCCCTA | TATGGACGAA | 1320 |
| ACACGTGCCA | TTGCCGGACA | ATTCAAAGAG | ANAGTGCTCG | GCTTCATCAG | CACGACCGGC | 1380 |
| CAGAAGGCTG | AAACTCTGAA | GCCGGCAGCC | ACGTCTGTGT | GGAACAAGGC | TGAGCAGTTC | 1440 |
| TGGNCCACAT | ACATGTGGAA | CTTCATCAGT | GGGATACAAT | AATAG | | 1485 |

(2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Cys Ala Arg Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr

1 10 15

Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala His Asp Val 20 25 30

Ile Ile Cys Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly 35 40 45

Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val 50 55 60

Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro 65 70 75 80

Asn Ile Glu Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr 85 90 95

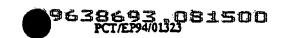
Gly Arg Ala Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile 100 105 110

Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr

Ser Leu Gly Val Asm Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala 130 135 140

| Va. 14 | l I1: | e Pro | Th: | Thi | : Gly 150 | Asç | Vàl | Val | . Val | Cys 155 | | The | . Yeb | Ala | Leu 160 |
|-----------|-------|------------|-----|------------|--------------|------|-------|-----|-------|------------|-----|------------|-------|-----|------------|
| | | | | 165 | , | | | | 170 | | | | | 175 | |
| | | | 100 | | | | | 185 | | | | | 190 | | |
| | | 193 | • | Val | | | 200 | | | | | 205 | | | |
| | -10 | , | |) Arg | | 215 | | | | | 220 | | | | |
| 445 | | | | Ser | 230 | | | | | 235 | • | | | | 240 |
| | | | | Cys 245 | | | | | 250 | | | | | 255 | |
| | | | 260 | Ala | | | | 265 | | | | | 270 | | • |
| | | 2/3 | | Phe | | | 280 | | | | | 2\$5 | | | |
| | 230 | | | Leu | | 295 | | | | | 300 | | | | |
| 202 | | | | Tyr | 310 | | | | | 315 | | | | | 320 |
| | | | | Asp 325 | | | | | 330 | | | | | 335 | |
| | | | 340 | Pro | | | | 345 | | | | | 350 | | |
| | | 355 | | Leu | | | 360 | | • | | | 365 | | | |
| | 370 | | | Leu | | 375 | | | | | 380 | | | | |
| 202 | | | | Ala | 390 | | | | | 395 | | | ٠ | | 400 |
| | | | | Arg 405 | | | | | 410 | | | | | 415 | |
| | | | 420 | Leu | | | | 425 | | | • | | 430 | | |
| Ala | Ser | Leu 435 | Pro | Tyr | Mec : | ysb. | Glu ' | Thr | Arg | Ala | | Ala 445 | Gly | Gln | Phe |

. .



Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu
450 455 460

Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe 465 470 475 480

Trp Xaa Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1485 base pairs
 - (B) TYPE: mucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1485

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

| TGTGCCAGGA | CCATCACCAC | CGGAGCTTCT | ATCACATACT | CCACTTACGG | CAAGTTCCTT | 60 |
|------------|------------|------------|------------|------------|------------|-----|
| GCTGATGGAG | GGTGTTCAGG | CGGCGCGTAT | GACGTGATCA | TATGCGACGA | GTGCCATTCC | 120 |
| CAGGACGCCA | CCACCATTCT | TGGGATAGGC | ACTGTCCTTG | ACCAGGCAGA | GACGGCTGGA | 180 |
| GCTAGGCTCG | TCGTCTTGGC | CACGGCCACC | CCTCCCGGCA | GTGTGACAAC | GCCCCACCCC | 240 |
| AACATCGAGG | AAGTGGCCCT | GCCTCAGGAG | GGGGAGGTTC | CCTTCTACGG | CAGAGCCATT | 300 |
| CCCCTTGCTT | TTATAAAGGG | TGGTAGGCAT | CTCATCTTCT | GCCATTCCAA | GAAAAAATGT | 360 |
| GATGAACTCG | CCAAGCAACT | GACCAGCCTG | GGCGTGAACG | CCGTGGCATA | TTATAGAGGT | 420 |
| CTAGACGTCG | CCGTCATCCC | CACAGCAGGA | GACGTGGTCG | TGTGCAGCAC | CGACGCGCTC | 480 |
| ATGACGGGAT | TCACCGGCGA | CTTTGATTCT | GTCATAGACT | GCAACTCCGC | CGTCACTCAG | 540 |
| ACGGTGGACT | TCAGTCTGGA | TCCCACTTTT | ACCATTGAGA | CTACCACAGT | GCCCCAGGAC | 600 |
| GCAGTGTCCA | GAAGCCAGCG | TAGGGGCCGC | ACGGGGAGAG | GTAGGCACGG | CATATACCGG | 660 |
| | CTGGAGAGAG | | | | | 720 |
| | | | | | | |
| TACGATGCCG | GATGTGCGTG | GTATGATCTG | ACTECTGEEG | AGACTACCGT | GAGGTTGCGC | 780 |
| GCTTACATAA | ACACCCCCGG | GCTCCCTGTC | TGTCAGGACC | ATTTGGAATT | CTGGGAGGGG | 840 |
| GTGTTCACGG | GGCTCACTÀA | CATCGACGCT | CACATGCTGT | CACAGACCAA | ACAGGGTGGG | 900 |
| GAGAATTTNC | CATACCTTGT | AGCGTACCAA | GCAACAGTCT | GTGTTCGCGC | GAAAGCGCCC | 960 |

1440

1485

CAGAAGGCTG AAACTCTGAA GCCGGCAGCC ACGTCTGTGT GGAACAAGGC TGAGCAGTTC

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 amino acids

TGGGCCACAT ACATGTGGAA CTTCATCAGC GGGATACAAT AATAG

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

Cys Ala Arg Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr 1 5 10 15

Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val 20 25 30

Ile Ile Cys Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly
35 40 45

Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val

Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro. His Pro 65 70 75 80

Asn Ile Glu Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr

Gly Arg Ala Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile

Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr 115 120 125

| | | | | | | | 257 | | | | | | | | |
|------------------------|------------|------------|------------|------------|------------|------------|--------------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Ser | Leu 130 | Gly | / Val | Asn | Ala | Val 135 | Ala | Tyr | Tyr | Arg | Gly 140 | Leu | Asp | Val | Ala |
| Val 145 | Ile | Pro | Thr | Ala | Gly 150 | Asp | Val | Val | Val | Суз 155 | Ser | Thr | Ąsp | Ala | Leu 160 |
| Met | Thr | Gly | Phe | Th: 165 | Gly | Asp | Phe | Asp | Ser 170 | Val | Ile | Asp | CÀR | Asn 175 | Ser |
| Ala | Val | Thr | Gln 180 | Thr | Val | Asp | Phe | Ser 185 | Leu | Asp | Pro | Thr | Phe 190 | Thr | Ile |
| Glu | Thr | Thr 195 | Thr | Val | Pro | Gla | Д Бр 200 | Ala | Val | Ser | Arg | Ser 205 | Gla | Arg | Arg |
| Gly | Arg 210 | Thr | Gly | Arg | Gly | Arg 215 | His | Gly | Ile | ıλ: | Arg 220 | Tyr | Val | Ser | Ala |
| Gly 225 | Glu | Arg | Xaa | Ser | Asp 230 | Met | Phe | λsp | Ser | Val 235 | Val | Leu | Cys | Glu | Cys 240 |
| Tyr | Asp | λla | Gly | Cys 245 | Ala | Trp | Tyr | Asp | Leu 250 | Thr | Pro | Ala | Glu | Thr 255 | Thr |
| Val | Arg | Leu | Arg 260 | λla | īyī | Ile | nak | Thr 265 | Pro | Gly | Leu | Pro | Val 270 | Cys | Gla |
| Asp | His | Leu 275 | Glu | Phe | Trp | Glu | Gly 280 | Val | Phe | Thr | Gly | Leu 285 | Thr | Asn | Ile |
| Asp | Ala 290 | His | Met | Leu | Ser | Gl= 295 | Thr | Lys | Gla | Gly | Gly 300 | Glu | Asa | Xaa | Pro |
| Ty r 305 | Leu | Val | Ala | TYT | Gla 319 | Ala | Thr | Val | Cys | Val 315 | Arg | Ala | ŗ'ns | Ala | Pro 320 |
| Pro | Pro | Ser | Trp | Asp 325 | Thr | Met | Trp | Lys | Cys 330 | Met | Leu | Arg | Leu | Lys 335 | Pro |
| Thr | Leu | Thr | Gly 340 | Pro | Thr | 510 | Leu | Leu 345 | | Arg | Leu | Gly | Pro | Val | Gln |

340 345 Let Tyr Arg Let Gly Pro Val Gln

Xaa Glu Ile Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys 355 360 365

Met Ser Ala Asp Leu Glu Val Ile Thr Xaa Thr Trp Val Leu Val Gly 370 375 380

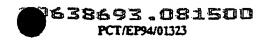
Gly Val Val Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val 385 390 395 400

Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro 405 410 415

Asp Arg Glu Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser 420 425 430

Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe

258



435 440 445

Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu 450 455 460

Thr Leu Lys Pr Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe 465 470 475 480

Try Ala Thr Tyr

- (2) INFORMATION FOR SEQ ID NO: 201:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..340
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 2..337
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:
- C TCC ACT GTG ACT GAG AGA GAC ATC AGG GTC GAA GAA GAA GTC TAT 46
 Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr
 1 5 10 15
- CAG TGT TGT GAT CTG GAG CCC GAG GCC CGC AAG GTA ATA ACC GCC CTC

 Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu

 20
 25
 30
- ACG GAG AGA CTC TAC GTG GGC GGC CCT ATG TAC AAT AGC AAG GGA GAC

 Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp

 40

 45
- CTT TGC GGG TAT CGC AGG TGC CGC GCA AGC GGC GTA TAT ACC ACC AGC
 Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser
 50 55 60
- TTC GGG AAC ACA CTG ACG TGC TAC CTT AAA GCC TCA GCA GCC ATC AGG
 Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg
 65 70 75
- GCT GCG GGG CTG AAG GAC TGC ACC ATG CTG GTT TGC GGT GAC GAC TTA Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu 80 90 95



GTC GTG ATC GCT GAA AGC GGT GGC GTC GAG GAG GAC AAG CGA GCC CTC 334
Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu
100 105 110

GGA GCT Gly Ala 340

- (2) INFORMATION FOR SEQ ID NO: 202:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln

1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asm Ser Lys Gly Asp Leu 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala 65 70 75 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85 90 95

Val Ile Ala Glu Ser Gly Gly Val Glu Asp Lys Arg Ala Leu Gly
100 105 110

Ala

- (2) INFORMATION FOR SEQ ID NO: 203:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

| 1 | ix | FEATURE : | |
|---|----|-----------|--|
| п | _ | FEMILIKE: | |

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide.

(B) LCCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

| C 1 | CC A Ser T | ca c | TG A | CT G | AA A lu A S | GA G K Ez | A DA I ça | TC A | ra A | TC G al G | AG G | AA G | AG G lu V | al T | AC YT 15 | 46 |
|------------------|------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|------------------|-------|
| CAG Gln | Cys | TGT Cys | GAC Asp | Leu 20 | GAG Glu | Bro CCI | GAA Glu | ACC Thr | CGC Arg 25 | Lys | GTA Val | ATA Ile | TCT Ser | GCC Ala 30 | CTC Leu | 94 |
| ACT | GAA Glu | AGA Arg | CTC Leu 35 | TAT Tyr | GTG Val | GGC Gly | GGT Gly | CCC Pro 40 | ATG Mec | CAC His | AAC Asa | AGC Ser | AGG Arg 45 | GGA Gly | GAC Asp | 142 |
| CTA Leu | TGC Cys | GGG Gly 50 | TAC Tyr | CGT Arg | AGA Azg | TGC Cys | CGC A2g 55 | GCG Ala | AGC Ser | GC | GTA Val | TAC Tyr 60 | ACC Thr | ACA Thr | AGC Ser | · 190 |
| TTC Phe | GGG Gly 65 | AAC Asn | ACT Thr | CTG Leu | ACG Thr | TGC Cys 70 | TTC Phe | CTC Leu | AAG Lys | GCC Ala | ACA Thr 75 | GCG Ala | GCC Ala | ACC Thr | AAA Lys | 238 |
| GCC Ala 80 | GCT Ala | GGC Gly | CTA Leu | aag Lys | GAC Asp 85 | TGC Cys | ACC Thr | ATG Met | TIG Leu | GTG Val 90 | TGT Cys | GGT Gly | GAC Asp | GAC Asp | TTA Leu 95 | 286 |
| GTC Val | GTT Val | ATC Ile | GCC Ala | GAA Glu 100 | AGC Ser | GAT Asp | GGT Gly | GTC Val | GAA Glu 105 | GAG Glu | GAC Asp | CGC | Arg | GCC Ala 110 | CTC Leu | 334 |
| GGA Gly | | | | | | | | | | | | | | | | 340 |

(2) INFORMATION FOR SEQ ID NO: 204:

- (1) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln 1 5 10 15

46 .

142

Cys Cys Asp Leu Glu Pro Glu Thr Arg Lys Val Ile Ser Ala Leu Thr 25 Glu Arg Leu Tyr Val Gly Gly Pro Met His Asa Ser Arg Gly Asp Leu 40 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe Gly Asn Thr Leu Thr Cys Phe Leu Lys Ala Thr Ala Ala Thr Lys Ala 70 Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Arg Ala Leu Gly 100 105 Ala (2) INFORMATION FOR SEQ ID NO: 205: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 340 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(ii) MOLECULE TYPE: cDNA

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

C TCC ACG GTG ACC GAA AGG GAT ATC AGG ACC GAG GAA GAG ATC TAC Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr 1 5 10 15

CAG TGC TGC GAC CTG GAG CCC GAA GCC CGC AAG GTG ATA TCC GCC CTA
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu
20 25 30

ACG GAA AGA CTC TAC GTG GGC GGT CCC ATG TAC AAC TCC AAG GGG GAC
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp
35 40 45

262

| CTA Leu | CÀZ | GGG Gly 50 | CAA Gln | CGG | AGG Arg | TGC Cys | CGC Arg 55 | GCA Ala | AGC Ser | GGG Gly | GTC Val | TAC Tyr 60 | ACC Thr | ACC Thr | AGC Ser | | 190 |
|------------------|-------------------|------------------|------------|-------------------|------------------|------------------|------------------|------------|-------------------|------------------|------------------|------------------|------------|-------------------|------------------|---|-----|
| TTC Phe | GGG GLY GGG | AAC Asn | ACT Thr | GTA Val | ACG Thr | TGT Cys 70 | TAT Tyr | CTC | AAG Lys | GCC Ala | G.T Val 75 | GC3 Ala | GCT Ala | ACT Thr | AGG Arg | | 238 |
| GCC Ala 80 | GCA Ala | Gly | CTG Leu | aaa Lys | GGT Gly 85 | TGC Cys | AGC Ser | ATG Met | CTG Leu | GTT Val 90 | C'a L'A | GGA Gly | GAC Asp | gac Asp | TTA Leu 95 | | 286 |
| GTC Val | GTC Val | ATC Ile | TGC Cys | GAG Glu 100 | AGC Ser | G1y GGC | GGC Gly | GTA Val | GAG Glu 105 | GAG Glu | gat Asp | GCA Ala | AGA Arg | GCC Ala 110 | CTC Leu | | 334 |
| CGA Atg | | | | | | | | | | | | | | | | • | 340 |

(2) INFORMATION FOR SEQ ID NO: 206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gln 1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg Ala 65 70 75 80

Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val

Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg

Ala

(2) INFORMATION FOR SEQ ID NO: 207:



| (i) SEQUENCE CHARACTERI | ISTICS . |
|-------------------------|----------|
|-------------------------|----------|

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: CDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

| C TCC ACG GTG ACT GAA AGG GAC ATT AGG GTC GAG GAA GAG ATC TAC Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Ile Tyr 1 5 10 15 | · 46 |
|--|------|
| CAG TGC TGT GAC CTG GAG CCC GAG GCA CGC AAG GTG ATA TCC GCT CTC Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu 20 25 30 | 94 |
| ACA GAA AGA CTC TAC AAG GGC GGC CCC ATG TAT AAC AGC AAG GGG GAC Thr Glu Arg Leu Tyr Lys Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp 35 40 45 | 142 |
| CTA TGC GGG CTT CGG AGG TGC CGC GCA AGC GGG GTA TAC ACC ACA AGC Leu Cys Gly Leu Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser 50 55 60 | 190 |
| TTC GGG AAC ACG GTG ACA TGC TAC CTT AAA GCC ACA GCA GCC ACC AGG Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg 65 70 75 | 238 |
| GCT GCA GGG CTG AAA GAT TGC ACT ATG CTG GTA TGC GGT GAC GAC TTA Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu 80 85 90 95 | 286 |
| GTC GTT ATT GCC GAA AGC GGT GGC GTG GAG GAG GAC GCC CGA GCC CTC Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu 100 105 110 | 334 |
| CGA GCC Arg Ala | 340 |

(2) INFORMATION FOR SEQ ID NO: 208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: procein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208: Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln

1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr

Glu Arg Leu Tyr Lys Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Leu Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe 50 55 60

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala 65 70 75 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg

Ala

- (2) INFORMATION FOR SEQ ID NO: 209:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..340
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

CCCCACCGTG ACNGAGAGGG ACNTCAGGGT CGAGGAAGAG GTCTATCAGT GCTGTAATCT

60

GGAGNCCGAT GNCCGCAAGG TCATCAACGC CCTCACAGAG AGACTCTACG TGGGCGGCCC

120

| GAGCATTGGC | ATAGACGASG | ACAAGCAAGC | CCTCCCERCT | | | 340 |
|------------|------------|------------|-------------|------------|------------|-----|
| CGCGGGCTTG | AAGGATTGCA | CCATGCTGGT | CTGCGGGIGAC | GACCTGGTTG | TCATTGCTGA | 300 |
| CACCACGAGC | TTCGGAAACA | CGCTGACTTG | CTACCTCAAA | GCCACAGCGG | CCACCAGGGC | 240 |
| TATGCACAAC | AGCAAGGGAG | ACCTGTGTGG | CATCOGTAGA | TGCCGCGCGA | GCGGCGTTTA | 180 |

- (2) INFORMATION FOR SEQ ID NO: 210:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

Pro Thr Val Thr Glu Arg Asp Xaa Arg Val Glu Glu Glu Val Tyr Glm

Cys Cys Asn Leu Glu Xaa Asp Xaa Arg Lys Val Ile Asn Ala Leu Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Ile Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe 50 55 60

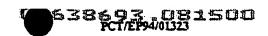
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala 65 70 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Ala Glu Ser Ile Gly Ile Asp Glu Asp Lys Gln Ala Leu Arg 100 105 110

Thr

- (2) INFORMATION FOR SEQ ID NO: 211:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA



| (: | iii | HYPOTHETICAL: | NO |
|----|-----|---------------|----|
| | | | |

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/REY: CDS
(B) LOCATION: 1.:340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

| | CTCGACTGTG | NCCGAGAGGG | ACATCAGGAC | AGAGGGAGAG | GTCTATCAGT | GTTGCGACCT | 60 |
|---|------------|------------|------------|------------|------------|------------|-----|
| | GGAACCGGAA | GCCCGCAAGG | TAATCACCGC | CCTCACTGAG | AGACTCTATG | TGGGCGGACC | 120 |
| 1 | CATGTTCAAC | AGCAAGGGAG | ACCTGTGCGG | ACAACGCCGG | TGCCGCGCAA | GCGGCGTGTT | 180 |
| 1 | CACCACCAGC | TTCGGGAACA | CACTGACGTG | СТАССТТААА | GCCACAGCTG | CTACTAGAGC | 240 |
| 2 | AGCCGGCTTA | AAAGATTGCA | CCATGCTGGT | CTGCGGTGAC | GACTTAGTCG | TTATTTCCGA | 300 |
| (| SAGCGCCGGT | GTGGAGGAGG | ATCCCANAAC | CCINCGACCI | | | 340 |

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

Ser Thr Val Xaa Glu Arg Asp Ile Arg Thr Glu Gly Glu Val Tyr Gln 1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Asp Leu 35 40 45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Phe 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala

286

| 65 | 70 | 75 | 80 | |
|---------------|------------------------|---------------------|----------------------|---|
| Ala Gly Leu L | 95 85 Ya Asp Cys | Val Cys Gly : 90 | Asp Asp Leu Va 95 | 1 |

Val Ile Ser Glu Ser Ala Gly Val Glu Glu Asp Pro Xaa Thr Xaa Arg

Pro

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 (B) LOCATION: 2..340
- (ix) FEATURE:

65

- (A) NAME/KEY: mat_peptide (B) LOCATION: 2...337
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

70

| | T GTT GAG GAG TCA ATT T g Val Glu Glu Ser Ile T 10 | |
|--------------------|--|-----|
| Gin Cys Cys Asp Le | AGA CAG GCC ATA AAG TCG Arg Gln Ala Ile Lys Ser 25 | Leu |
| | CTG ACT AAT TCA AAG GGG Leu Thr Asn Ser Lys Gly 45 | |
| | AGC GGC GTG CTG ACG ACC Ser Gly Val Leu Thr Thr 60 | |
| _ | ANG GCC TCT GCA GCC TGT Lys Ala Ser Ala Ala Cys | |

SUBSTITUTE SHEET (RULE 26)

GCT GCG AAG CTC CAG GAC TGC ACG ATG CTC GTG TGC GGG GAC GAC CTT

Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu 80 85 90 95

CGA GTC
Arg Val

- (2) INFORMATION FOR SEQ ID NO: 214:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln
1 10 15

Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu Thr 20 25 30

Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg Ala 65 70 75 80

Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu Arg 100 105 110

Val

- (2) INFORMATION FOR SEQ ID NO: 215:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: CONA

| (iii) | HYPOTHETICAL: | NO |
|-------|---------------|----|
|-------|---------------|----|

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat_peptide (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

| C T | CA A er T 1 | CC G | TC A | CG Gi hr Gi | AG AG Lu Ai 5 | GG GI | AT A' sp I | TA Ad le Ai | rg Ti | CA G hr G 10 | AA G lu G | AA To lu Si | CC A' er I | TA T | at Yt Ls | - 46 |
|------------|-------------------|------------|------------|----------------|---------------------|------------|---------------|----------------|------------|--------------------|--------------|----------------|---------------|------------|----------------|------|
| CAA Gln | GCT Ala | TGT Cys | TCC Ser | CTG Leu | CCC CCC | CAA Gln | GAG Glu | GCC Ala | AGA Arg | ACT Thr | GTC Val | ATA Ile | CÁC Hìs | TCG Ser | CTC Leu | 94 |
| | | | | 20 | | | | | 25 | | | | | 3 C | | |
| ACC | GAG | AGA | CTC | TAC | GTG | GGA | GGG | CCC | ATG | ATA | AAC | AGC | AAA | GGG | CAA | 142 |
| Thr | Glu | Arg | Leu 35 | Tyr | Vai | Gly | Gly | Pro 40 | Met | Ile | Asa | Ser | Lys 45 | Gly | Gln | |
| TCC | TGC | GGT | TAC | AGG | CGT | TGC | CGC | GCA | AGC | GGT | GII | TTC | ACC | ACC | AGC | 190 |
| Ser | Cys | Gly | Tyr | Arg | Arg | Cys | Arg | Ala | Ser | Gly | Val | Phe | Thr | Thr | Ser | |
| | | 50 | | | | | 55 | | | | | 60 | | | | |
| | | | | | | | | | | | | | | TGT | | 238 |
| Met | 65 65 | Asn | Thr | Met | Thr | Cys 70 | Tyr | Ile | Lys | Ala | Leu 75 | Ala | Ala | Cys | Ļvs | |
| GCC | GCA | GGG | ATC | GTG | GAC | ccc | GTC | ATG | CTG | GTG | TGT | GGA | GAC | GAC | CTG | 286 |
| Ala | Ala | Gly | Ile | Val | Asp | Pro | Val | Met | Leu | Val | Cys | Gly | qaA | Asp | Leu | |
| 80 | | | | | 85 | | | | | 90 | | | | | 95 | |
| GTC | GTC | ATC | TCG | GAG | AGC | CAG | GGT | AAC | GAG | GAG | GAC | GAG | CGA | AAC | CTG | 334 |
| Val | Val | Ile | Ser | | Ser | Gln | Gly | Asn | | Glu | Asp | Glu | Arg | Asn | Leu | |
| | | | | 100 | | | | | 105 | | | | | 110 | | |
| | GCT | | | | | | | | | | | | | | | 340 |
| Arg | Ala | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein



46

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln
1 5 10 15

Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu Thr 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln Ser 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met 50 55 60

Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys Ala 65 70 75 80

Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu Arg

Ala

(2) INFORMATION FOR SEQ ID NC: 217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..340
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 2..340
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:
- C TCG ACT GTC ACT GAA CAG GAC ATC AGG GTG GAA GAG GAG ATA TAT Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr 1 5 10 15
- CAA TGC TGC AAC CTT GAA CCG GAG GCC AGG AAA GTG ATC TCC TCC CTC Gln Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu

| | • | • | | 20 | | | | | 25 | | | | | 30 | | | |
|----------------------|----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|---|-----|
| ACG G | | | | | | | | | | | | | | | | ٠ | 142 |
| CAG T | | | | | | | | | | | | | | | | | 190 |
| TTT G | | | | | | | | | | | | | | | | | 238 |
| GCC G Ala A 80 | Ца | Gly | Leu | Arg | Asn 85 | Pro | qzA | Phe | Leu | Val 90 | Cys | Gly | Asp | Asp | Leu 95 | | 286 |
| GTC G Val V | | | | | | | | Va. | | | | | | | | • | 334 |
| AGA G | | | | | | | | | | | | | | | | | 340 |

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERÍSTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln
1 5 10 15

Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu Thr 20 25 30

Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala Gln
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe

Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Thr Ala Ala Lys Ala 65 70 75 80

Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu Val 85 90 95

Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala Leu Arg
100 105 110

Ala

- (2) INFORMATION FOR SEQ ID NO: 219:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

Arg Ser Glu Gly Arg Thr Ser Trp Ala Gln
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 220:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

Arg Ser Glu Gly Arg Thr Ser Trp Ala Gln
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 221:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

Arg Thr Glu Gly Arg Thr Ser Trp Ala Gln
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 222:
 - (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 629 base pairs

| (B) | TYPE: nucleic | acid |
|-----|----------------|--------|
| (C) | STRANDEDNESS: | single |
| (D) | TOPOLOGY: line | ear |

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(ix) FEATURE:

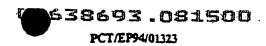
(A) NAME/KEY: CDS
(B) LOCATION: 3..629

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 3..629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

| | (XI | 1 32 | Quan | (= 0 | esca. | 12110 | M: 3 | ، يند | טא ענ | | • • | | | | | |
|-----|------|------------|-------------------|--------------|----------|----------------|------|-------|------------|-------|-----------|-----|------------|-------|-----------|-----|
| | | | | | | GTC 1 | | | | | | | | | | 47 |
| | 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| | | | | | | AAG Lys | | | | | | | | Phe | | 95 |
| | | | | 20 | | | | | 25 | | | | | 30 | | |
| ACT | GCC | TAC | : כאא | GCC | ACT | GTG | TGC | GCT | CGC | GCG | CAG | GCT | CCT | CCC | cca | 143 |
| | | | | | | Val | | Aia | | | | | 510 | | | |
| | | | 35 | + | | | | 40 | | | | | 45 | | | |
| | | | | | | AAG | | | | | | | | | | 191 |
| Ser | Trp | _ | | Met | Trp | Lys | | Leu | Val | Arg | Leu | | Pro | Thr | Leu | |
| | | 50 |) | | | | 55 | | | | | 60 | | | | |
| CAT | GGA | cca | ACC | CCI | CTI | CTA | TAT | CGG | TTG | GGG | CCT | GTC | CAA | aat | GAA | 239 |
| His | - | | The | Pro | Leu | Leu | Tyr | Arg | Leu | Gly | Pro 75 | Val | Gln | Asn | Glu | |
| | 65 | • | | | | 70 | | | | | . /3 | | | | | |
| ATC | TGC | TTO | ac: | CAC | : cc | ATC | ACA | AAA | TAC | ATC | ATG | GCA | TGC | ATG | TCA | 287 |
| | - | Le | Th: | His | 85 88 | Ile | Thr | Lys | Ty | Ile | Met | Ala | Cys | Met | 5er 95 | |
| 80 | 1 | | | | 6: | • | | | | ,, | | | | | - | |
| GC1 | GA1 | CI | G GAJ | A GT | ACC | ACC | AGC | ACC | TGG | GTT | TTG | CTT | GGA | GGG | GTC | 335 |
| Ala | Ası | Le | u Gl | ı Val 100 | | r Thr | Ser | The | 105 305 | | Leu | Leu | GIY | 110 | | |
| | | | | | | | | | | | | | | | | |
| CTC | : GC | GC | CCT | A GCC | G GC | C TAC | TGC | TIG | TCA | GTC | GGT | TGT | GTT | GIG | ATT | 383 |
| Let | Ala | a Al | a Le ¹ | | a Ali | a Tyr | CAa | 120 | | AST | GIĄ | Cys | 125 | VA. | 116 | |
| | | | | | | | | - | | | | | | | | 433 |
| GTO | GG | r ca | TAT | C GAG | G CT | G GGG u Gly | GGC | AAC | CCG | GCA | ATC | GTI | CCA Pro | . GAC | LVS | 431 |
| va. | r GT | y H1 13 | | e CT | r re | a GIA | 139 | | , F.C | , WTQ | TIE | 140 | | ړ ده | . 2,0 | |
| | | | | | | | | | | | | | | | | |



| GAG Glu | GTG Val 145 | TTG | TAT Tyr | GJ II | CAA | TAC Ty= 150 | GAT Asp | GAG Glu | ATG Net | Glu | GAG Glu 155 | Cys Cys | TCA Ser | CAA Gln | GCT Ala | | 479 |
|-------------------|-------------------|------------|-------------------|-------------------|--------------------|-------------------|------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|-------------------|-------------------|---|------|
| GCC Ala 160 | CCA Pro | TAT Tyr | ATC Ile | GJu GJu | CAA Gl:: 165 | GCT Ala | CAG Gln | GTA Val | ATA Ile | GCT Ala 170 | CAC His | CAG Gln | TTC Phe | AAG Lys | GAA Glu 175 | | \$27 |
| AAA Lys | GTC Val | CTT Leu | GGA Gly | TTG Leu 180 | CTG Leu | CAG Gln | CGA | GCC Ala | ACC Thr 185 | CAA Glm | CAA Gln | CAA Gln | GCT Ala | GTC Val 190 | ATT Ile | ; | \$75 |
| GAG Glu | CCC Pro | ATA Ile | GTA Val 195 | ACT Thr | ACC Thr | aac Asi | TGG Trp | CAA Gln 200 | aag Lys | CTT Leu | GAG Glu | GCC Ala | TTT Phe 205 | TGG TYP | CAC His | (| 623 |
| AAG Lys | | | | | | - | | | | | | | | | | | 529 |

(2) INFORMATION FOR SEQ ID NO: 223:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 209 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 1 5 10 15

Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr 20 25 30

Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser 35 40 45

Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His 50 55 60

Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile 65 70 75 80

Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 85 90 95

Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu Gly Gly Val Leu
100 105 110

Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys Val Val Ile Val

Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys Glu 130 135 140



Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys Ser Gln Ala Ala 145 150 155 160

Pr Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln Phe Lys Glu Lys 165 170 175

Val Leu Gly Leu Leu Gin Arg Ala Thr Gln Gln Gln Ala Val Ile Glu 180 185 190

Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala Phe Trp His Lys
195 200 205

His

- (2) INFORMATION FOR SEQ ID NO: 224:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: Peptide
 - (B) LOCATION: 2..12
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

Ile His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile

1 5 10

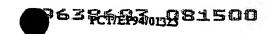
- (2) INFORMATION FOR SEQ ID NO: 225:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - . (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 5:
 - (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:
- Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile
- (2) INFORMATION FOR SEQ ID NO: 227:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amine acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:
 - Val Asn Tyr His Asn Thr Ser Gly Ile Tyr His Leu 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 228:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:
 - Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val 1 10
- (2) INFORMATION FOR SEQ ID NO: 229:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val

1 5 10

- (2) INFORMATION FOR SEQ ID NO: 230:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

Ile His Tyr Arg Asn Ala Ser Asp Gly Tyr Tyr Ile
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 231:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

Leu Gln Val Lys Asn Thr Ser Ser Ser Tyr Met Val

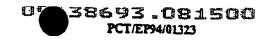
- (2) INFORMATION FOR SEQ ID NO: 232:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Val Trp Gln Leu Arg Ala Ile Val Leu His Val 1 5 10

(2) INFORMATION FOR SEO ID NO: 233:



- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MCLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:
- Val Tyr Glu Ala Asp Tyr His Ile Leu His Leu 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 234:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:
 - Val Tyr Glu Thr Asp Asn His Ile Leu His Leu 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 235:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTE: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:
 - Val Tyr Glu Thr Glu Asn His Ile Leu His Leu 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 236:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (3) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Val Phe Glu Thr Val His His Ile Leu His Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 237:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPCLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

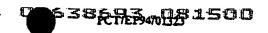
Val Phe Glu Thr Glu His His Ile Leu His Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 238:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

Val Phe Glu Thr Asp His His Ile Met His Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 239:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Val Tyr Glu Thr Glu Asn His Ile Leu His Leu 1 5 10



- (2) INFORMATION FOR SEQ ID NO: 240:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Val Tyr Glu Ala Asp Ala Leu Ile Leu His Ala 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 241:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Val Gin Asp Gly Asn Thr Ser Ala Cys Trp Thr Pro Val 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 242:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242: Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu 1 5 10
- (2) INFORMATION FOR SEQ ID NO: 243:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 244:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: pertide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Val Arg Thr Gly Asm Glm Ser Arg Cys Trp Val Ala Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 245:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 246:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:
 - -Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu

1 5 10

- (2) INFORMATION FOR SEQ ID NO: 247:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Val Lys Thr Gly Asn Ser Val Arg Cys Trp Ile Pro Leu 1 5 10

- (2) INFORMATION FOR SEQ ID NG: 248:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Val Lys Thr Gly Asn Val Ser Arg Cys Trp Ile Ser Leu
1 5

- (2) INFORMATION FOR SEQ ID NG: 249:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

Val Arg Lys Asp Asm Val Ser Arg Cys Trp Val Glm Ile
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 250:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid



- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

Ala Pro Ser Phe Gly Ala Val Thr Ala Pro
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 251:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTE: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Val Ser Gln Pro Gly Ala Leu Thr Lys Gly
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 252:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252;

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 253:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:



Ala Pro Tyr Ile Gly Ala Pro Val Glu Ser
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 254:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTE: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Ala Gln His Leu Asn Ala Pro Leu Glu Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 255:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Ser Pro Tyr Val Gly Ala Pro Leu Glu Pro 1 5 10

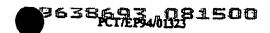
- (2) INFORMATION FOR SEQ ID NO: 256:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Ser Pro Tyr Ala Gly Ala Pro Leu Glu Pro 1 5 10

(2) INFORMATION FOR SEQ ID NO: 257:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids



- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Ala Pro Tyr Leu Gly Ala Pro Leu Glu Ser
1 5 10

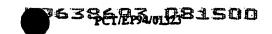
- (2) INFORMATION FOR SEQ ID NO: 258:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Ala Pro Tyr Leu Gly Ala Pro Leu Glu Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 259:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (3) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Ala Pro Tyr Val Gly Ala Pro Leu Glu Ser
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 260:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Asn Val Pro Tyr Leu Gly Ala Pr Leu Thr Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 251:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULZ TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Ala Pro His Leu Arg Ala Pro Leu Ser Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 252:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Ala Pro Tyr Leu Gly Ala Pro Leu Thr Ser
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 263:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids.
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Arg Pro Arg Gln His Ala Thr Val Gln Asp 1 5 10

(2) INFORMATION FOR SEQ ID NO: 254:



- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

Ser Pro Gln His His Lys Phe Val Gln Asp 1 5 10

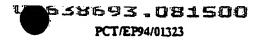
- (2) INFORMATION FOR SEQ ID NO: 265:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

Arg Pro Arg Arg Leu Trp Thr Thr Gln Glu
1 S 10

- (2) INFORMATION FOR SEQ ID NO: 266:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

Pro Pro Arg Ile His Glu Thr Thr Gln Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 267:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear



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- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

Thr Ile Ser Tyr Ala Asn Gly Ser Gly Pro Ser Asp Asp Lys
1 5 10

- (2) INFORMATION FOR SEQ ID NO: 268:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (3) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - ' (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Ser Arg Arg Gln Pro Ile Pro Arg Ala Arg Arg Thr Glu Gly Arg Ser 1 5 10

. Trp Ala Gla

- (2) INFORMATION FOR SEQ ID NO: 269:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1443
 - (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 1..1443
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

ACC ATC ACC ACC GGA GCT TCT ATC ACA TAC TCC ACT TAC GGC AAG TTC Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe

289

| | | | | _ | | | | | | | | | | | | |
|------------|------|-------------------------|--------------------|-----|-------------|-----|-------------|------------|------|--------|-----------|------|------|------|-----|-------|
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| CII | GCT | GAT | GGA | GGG | TGT | TCA | GGC | GGC | GCG | TAT | GAC | GTG | ATC | ATA | TGC | 96 |
| Leu | Ala | Asp | Gly | Gly | Cys | Ser | Gly | Gly | Ala | Tyr | Asp | Val | Ile | Ile | Суз | - |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| GAC | GAG | TGC | CAT | TCC | CAG | GZC | ccc | acc | 3.00 | محد لا | | | 3773 | | | • • • |
| Ast | Giu | Cvs | His | Ser | Gin | Aso | Ala | The | The | TI. | T.eu | GIV | WIW. | GUC | ACT | 144 |
| • | | 35 | | | | | 40 | •••• | | | 500 | 45 | | G±3 | | |
| | | | | | | | | | | | | | | | | |
| GIC | CII | GAC | CAG | GCA | GAG | ACG | GCT | GGA | GCT | AGG | CIC | GTC | GTC | TTG | GCC | 192 |
| Agt | 50 | ASŞ | Gln | ALA | GIU | SS | ALA | GLY | ALA | yrg | Leu 60 | Val | Val | Leu | Ala | |
| | • | | | | | | | | | | 90 | | | | | |
| ACG | GCC | ACC | CCT | CCC | GGC | AGT | GTG | ACA | ACG | ccc | CAC | CCC | AAC | ATC | GAG | 240 |
| Thr | Ala | Thr | Pro | Pro | Gly | Ser | Val | Thr | Thr | Pro | His | Pro | Asr. | Ile | Glu | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| 633 | GTG | CCC | CTG | | C3G | GNG | ccc | C3C | | | - | m) a | | | | |
| Glu | Val | Ala | Leu | Pro | Gla | Glu | Glv | Glu | Val | Pro | Phe | TVY | GGC | AGA | Bla | 288 |
| | | | | 85 | | | 2 | | 90 | ••• | • • • • • | •,,• | 4-, | 95 | ~~~ | |
| | | | | | | | | | | | | | | | | |
| ATT | CCC | CII | GCT | TIT | ATA | AAG | GGT | GGT | AGG | CAT | CTC | ATC | TTC | TGC | CAT | 336 |
| TIE | PIO | rea | Ala 100 | hue | TTE | rys | GIÅ | G17 105 | | His | Leu | Ile | | Cys | His | |
| | | | 100 | | | | | 103 | | | | | 110 | | | |
| TCC | AAG | $\lambda\lambda\lambda$ | AAA | TGT | GAT | GAA | CIC | GCC | AAG | CAA | CTG | ACC | AGC | CTG | GGC | 384 |
| Ser | Lys | Lys | Lys | Cys | Asp | Glu | Leu | Ala | Lys | Gln | Leu | Thr | Ser | Leu. | Gly | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| GTG | AAC | GCC | GTG | GCZ | тат | ጥኋም | AG 3 | CCT | دجے | Gac | GTC | 000 | a== | | ccc | 432 |
| Val | Asn | Aia | Val | Ala | Tyr | Tyr | Arq | Glv | Leu | ASD | Val | Ala | Val | Ile | Pro | 432 |
| | 130 | | | | • | 135 | • | • | | | 140 | | | | | • |
| | | | | | | | | | | | | | | | | |
| ACA Th- | GCA | GGA | GAC As p | GTG | GTC | GTG | TGC | AGC | ACC | GAC | GCG | CTC | ATG | ACG | GGA | 480 |
| 145 | 7-0 | GLY | vač | Vai | 150 | VAI | Cys | ser | Inr | 155 | ATZ | rea | Mec | Thr | 160 | |
| | | | | | | | | | | | | | | | 100 | |
| TTC | ACC | GGC | GAC | TIT | GAT | TCT | GTC | ATA | GAC | TGC | AAC | TCC | GCC | GTC | ACT | 528 |
| Phe | Thr | Gly | Asp | | Asp | Ser | Val | Ile | | Cys | Asn | Ser | Ala | Val | Thr | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| CAG | ACG | GTG | GAC | TTC | AGT | CTG | GAT | ccc | ACT | TTT | ACC | ATŤ | GZG | ACT | ACC | 576 |
| | | | Asp | | | | | | | | | | | | | 3.0 |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| 202 | carc | | CNC | ~ ~ | CO 3 | ~~~ | *** | | | | | | | | | |
| Thr | Val | Pro | CAG Gln | Asn | Ala | Val | Ser | AGA | AGC | CAG | CGT | AGG | GGC | CGC | ACG | 624 |
| •••• | | 195 | U | ກວວ | 724 | V4. | 200 | ~3 | 361 | GIII | ALG | 205 | Gry | Aig | THE | |
| | | | | | | | | | | | | | | | | |
| GGG | AGA | GGT | AGG | CAC | GGC | ATA | TAC | CGG | TAT | GTC | TCG | GCT | GGA | GλG | AGA | 672 |
| Gly | | Gly | Arg | His | Gly | | Tyr | Arg | Tyr | Val | | Ala | Gly | Glu | Arg | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| CCG | TCT | GAC | ATG | TTC | GAC | TCC | GTG | GTG | CTC | TGT | GAG | TGC | TAC | GAT | GCC | 720 |
| Pro | Ser | Asp | Met | Phe | Asp | Ser | Val | Val | Leu | Cys | Glu | Суз | Ty | Asp | Ala | |
| 225 | | | | | 230 | | | | | 235 | | • | | - | 240 | |

| GG; G1; | TGI Cys | GCG Ala | TGG TEP | TAT Ty= 245 | GAT Asp | CTG Leu | ACT Thr | Pro | GCC Ala 250 | GAG Glu | ACT Thr | ACC Thr | GTG Val | AGG Arg 255 | TTG Leu | 768 |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| CG(Arg | GCT Ala | TAC | Ile 260 | AAC Asn | ACC Thr | CCC | GGG Gly | CTC Leu 265 | Sz: CC: | GTC Val | Càr ICI | CAG Gln | GAC Asp 270 | CAT His | TTG Leu | 816 |
| GA: | TTC Phe | TGG Trp 275 | Glu | GGG Gly | GTG Val | TTC Phe | ACG Thr 280 | GGG Gly | CTC | act The | AAC Asn | ATC Ile 285 | GAC Asp | GCT Ala | CAC His | 864 |
| ATC Met | CTG Leu 290 | TCA Ser | CAG Gl:: | ACC Thr | aaa Lys | CAG Gln 295 | GGT Gly | GCG GCG | GJ:1 GAG | aat Asd | TTC Phe 300 | CCA Pro | TAC Tyr | CTT Leu | GTA Val | 912 |
| Ala 305 | Tyr | Gln | Ala | Thr | GTC Val 310 | Суѕ | Val | yzg | ۸ia | Lys | Ala | Pro | Pro | Pro | Ser 320 | 960 |
| Trp | GAC Asp | ACA Thr | ATG Met | TGG Trp 325 | AXA Lys | TGC Cys | ATG Met | CTC | CGT 330 | CTC | aaa Lys | CCG Pro | ACT Thr | TTA Leu 325 | ACT Thr | 1008 |
| GGC | CCT Pro | ACT Thr | CCC Pro 340 | CTC Leu | TTG Leu | TAC Tyr | AGG Arg | CTG Leu 345 | GGG Gly | 220 220 | GTC Val | CAG Glm | AAT Asn 350 | GAG Glu | ATC Ile | 1056 |
| ACA Thr | CTG Leu | ACG Thr 355 | CAC His | CCC Pro | ATC Ile | ACC Thr | AAG Lys | TAC TYT | ATT Ile | ATG Met | GCT Ala | TGC Cys 363 | ATG Met | TCT Ser | GCG Ala | 1104 |
| GAC Asp | TTG Leu 370 | GAG Glu | GTC Val | ATT Ile | ACC Thr | AGC Ser 375 | ACT The | TGG Tap | GTT Val | CTG Leu | GTG Val 330 | GGG | GGC Gly | GTT Val | GTG Val | 1152 |
| GCG Ala 385 | Ala | CTG Leu | GCG Ala | GCC Ala | TAC Tyr 390 | TGC Cys | TTG Leu | ACG Thr | GTG Val | GGT Gly 395 | TCG Ser | GTA Val | GCC Ala | ATA Ile | GTC Val 400 | 1200 |
| GGT Gly | AGG Arg | ATC Ile | ATC Ile | CTC Leu 405 | TCT Ser | Gly | Lys | 510 | GCC Ala 410 | Ile | ATT Ile | CCC | Asp | AGG Arg 415 | Glu | 1248 |
| GCA Ala | TTA Leu | TAC Tyr | CAG Glm 420 | Gln | TTT Phe | GAT Asp | GAG Glu | ATG Met 425 | GAG Glu | GAG Glu | TGC Cys | TCG Ser | GCC Ala 430 | TCG Ser | TTG Leu | 1296 |
| CCC | TAT Tyr | ATG Met 435 | GAC Asp | GAG Glu | ACA Thr | Arg | GCC Ala 440 | ATT Ile | GCC Ala | GGA Gly | CAA Gln | TTC Phe 445 | AAA Lys | GAG Glu | AAA Lys | 1344 |
| GTG Val | CTC Leu 450 | GGC Gly | TTC Phe | ATC Ile | AGC Ser | ACG Thr 455 | acc Thr | G17 GGC | CAG Gln | aag Lys | GCT Ala 460 | GAA Glu | ACT Thr | CTG Leu | aag Lys | 1392 |
| CCG Pro 465 | GCA Ala | GCC Ala | ACG Thr | TCT Ser | GTG Val 470 | TGG Trp | AAC Asn | AAG Lys | GCT Ala | GAG Glu 475 | CAG Gln | TTC Phe | TGG Trp | GCC Ala | ACA Thr 490 | 1440 |

TAC Tyr

1443

- (2) INFORMATION FOR SEQ ID NO: 270:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 481 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NG: 270:

Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe
1 5 10 15

Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys
20 25 30

Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr
35 40 45

Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala 50 60

Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asm Ile Glu 65 70 75 80 Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala

Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His

Ser Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr Ser Leu Gly
115 120 125

Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala Val Ile Pro 130 135 140

Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu Met Thr Gly
145 150 155 160

Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser Ala Val Thr

Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr 180 195 190

Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr . 195 200 205

Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala Gly Glu Arg 210 215 220

Pro Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys Tyr Asp Ala

292

225 230 235 Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr Val Arg Leu 245 250 Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 260 265 Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile Asp Ala His Met Leu Ser Gln Thr Lys Gln Gly Glu Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro Pro Pro Ser Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro Thr Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile 345 Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val 375 Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys 455

Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys

Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Ala Thr 470

Tyr